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Bowman,



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OM nucleic - nucleic search, using sw model

Run on:

August 6, 2005, 09:58:01; Search time 1445 Seconds (without alignments) 670.660 Million cell updates/sec

US-10-773-678-342 20 1 gactcttgcaggaagcggct 20 Title: Perfect score: Seguence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4708233 segs, 24227607955 residues Searched:

790860 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

GenEmbl:* Database :

6: 7: 88: 10: 11: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AR120998 Sequence	BD272619 Antisense	AR531367 Sequence	L24340 Dog (Clone:	BD228539 IL-17 hom	AR359764 Sequence	CQ798932 Sequence	A89364 Sequence 15	AX672730 Sequence	AX762313 Sequence	BD066877 An antise	AX117443 Sequence	AR098941 Sequence	AR164768 Sequence	BD222879 KVLQT1-QT	I79781 Sequence 77	AR218732 Sequence	AR223147 Sequence	AR229909 Sequence
SUMMARIES	ΩΙ	AR120998	BD272619	AR531367	DOGP45501	BD228539	AR359764	CQ798932	A89364	AX672730	AX762313	BD066877	AX117443	AR098941	AR164768	BD222879	179781	AR218732	AR223147	AR229909
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	Query Match Length DB	20	20	20	19	20	20	20	17	17	17	17	18	20	20	20	20	20	20	20
de	Query	70.0	70.0	70.0	65.0	64.0	64.0	63.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0
	Score	14	14	14	13	12.8	12.8	12.6	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4
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20 12.4 62. 22 12.2 61. 24 12.2 61. 25 12.2 61. 26 12.2 61. 27 12.2 61. 27 12.2 61. 28 12.2 61. 29 11.8 59. 31 11.8 59.	C 32 11.8 59.0 C 334 11.8 59.0 C 335 11.8 59.0 C 336 11.8 59.0 C 337 11.8 59.0 C 441 11.6 58.0 C 54 68.0 C 54 88.0 C 55 11.6 58.0 C 55 11.6 58.0 C 55 11.6 58.0 C 56 11.6 58.0 C 57 11.6 58.0 C 68 11.6 58.0 C 69 11.6 58.0 C 69 11.6 58.0 C 69 11.6 58.0 C 60 11.6 68.0 C 60 11.6 6	55 11.2 56. 67 11.2 56. 88 11.2 56. 90 11.2 56. 11.2 56. 11.2 56. 11.2 56.

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1 (Dases 1 to 19)
Ostrander, B.A., Mapa, F.A., Yee, M. and Rine, J.
One hundred and one new simple sequence repeat-based markers for the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA.
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
Seattle, WA 98104, USA
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Buffer: PCR buffer (Perkin-Black Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing:
Polymerization: 74 degrees C for 1.00 minutes
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Patent: US 6727064-A 19 27-APR-2004;
Location/Qualifiers
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                                                                                Query Match 70.0%; Score 14; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 9.7e+04; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%; Score 14; DB 6; Length 20; 100.0%; Pred. No. 9.7e+04; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    linear
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L24340
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PCR identification; PCR primer; STS.
1 of 2
Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                  AR531367 20 bp 1 Sequence 19 from patent US 6727064.
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/organism="unknown"
/wol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Karras, J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
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Best Local Similarity
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DOGP45501
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
FEATURES
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TITLE
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PUBMED
COMMENT
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SEGMENT
SOURCE
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AR531367
LOCUS
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Antisense oligonucleotide modulation of STAT3 expression.
BD272619
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                 AR464438 Sequence
AX728547 Sequence
AX760524 Sequence
BD244848 Polynucle
BD244849 Polynucle
AX023724 Sequence
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                                                                                                                                                  AX023725 Sequence
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PD 10-DEC-2002

PR 08-APR-1399 US 09/288461

PI JAMES G RARRAS

PC 122115/09, A61R31/711, A61R48/00, A61P29/00, A61P29/00, A61P29/00, A61P3/00, C122115/09, C122115/09, C122115/09, C122115/09, C122115/09, A61P3/09, C122115/09, A61P3/09, C122115/09, A61P3/09, C122115/09, A61P3/09, A61P3/09, C122115/09, A61P3/09, C122115/09, A61P3/09, A61
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                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense modulation of stat3 expression
Patent: US 6159694-A 19 12-DEC-2000;
Location/Qualifiers
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/organism="synthetic construct"
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                                                                                                                                                                                                                                                                                                                    AR120998 20 bp 1
Sequence 19 from patent US 6159694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
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                                                                                                                                                                                                                 ALIGNMENTS
                                                             AX760524
BD244848
BD244849
AX023724
                        AR464438
                                           AX728547
                                                                                                                                                  AX023725
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JP 2002541784-A/19.
synthetic construct
synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.
1 (bases 1 to 20)
Karras, J.G.
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  Unknown.
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  DEFINITION
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JOURNAL
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AUTHORS
TITLE
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BD272619
LOCUS
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FEATURES

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PAT 22-JAN-2000
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    .20
    /organism="synthetic construct"
    /mol Lype="unassigned DNA"
    /db xref="taxon:32630"
    /noce="Artificially synthesized primer sequence for RT-PCR"

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Method for diagnosing pancreatic cancer
Patent: WO 2004031412-A 13 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
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Gatanaga, T. and Granger, G.A. .
Tumor necrosis factor receptor releasing enzyme
Patent: US 659346-A 134 15-UUL-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%; Score 12.8; DB 6; 87.5%; Pred. No. 3.7e+05;
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Sequence 13 from Patent WO2004031412.
CQ798932
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Sequence 1512 from Patent WO9833904.
A89364
          20 bp Di
Sequence 134 from patent US 6593456.
AR359764
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/organism="unknown"
/mol_type="genomic DNA"
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1 (bases 1 to 17)
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                                                                                                                                                                                                     Unclassified.
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Matches 14; Conserv
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SOURCE
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1 (bases 1 to 20)

Chen, J., Filvaroff, E., Goddard, A., Gurney, A.L., Li, H. and Wood, W.I.
IL-17 homologous polypeptide and its application to remedy

Batent: JP 2002515246-A 134 28-MAY-2002;

GENENTECH INC
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Strandedness: Single;

Strandedness: Single;

Topology: Linear;

Topolog
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PN 2002515246-A/134
PD 28-MAY-2005
PP 14-MAY-1999 JP 2000549734
PR 15-MAY-1998 US 60/085579,23-DEC-1998 US 60/113621 PI
JIAN CHEN, ELLEN FILVAROPF, AUDLEY GODDARD, AUSTIN L GURNEY, PI
HANZHONG LI,
PI WILLIAM I WOOD
PC CI2NIS/09, A61K38/21, A61K45/00, A61P19/00, C07K14/52, C07K16/24,
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                                                                          1. .19 // Caranism="Canis familiaris" / organism="Canis familiaris" / db Arsef="taxon:9615" / tissue_type="spleen" / dis vatage="adult" / tissue_lib="E. Ostrander, in pBluescript+" 1. .19
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                                                                                                                                                                                                                                                                                                                                      ch 65.0%; Score 13; DB 4; Length 19; l Similarity 100.0%; Pred. No. 3e+05; 13; Conservative 0; Mismatches 0; Indels
  PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
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/organism="unidentified"
/mol_type="genomic DNA"
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JP 2002515246-A/134.
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PC C12N15/09, A61R38
PC C12N1/19, C12N1/2
, C12Q1/68, C12N15/00,
PC Strandedness: Si
CC Strandedness: Si
CC Topology: Linear
CC IL-17 homologous
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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FEATURES

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PAT 27-AUG-2002
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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonuclectide preparation method
Patent: JP 2001511000-A 1512 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OP-201511000-A/1512
OP-AUG-2001
30-JAN-1998 JP 1998532533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
CI2N15/11, CO7H21/04, A61K71/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%; Score 12.4; DB 6; Length 17; 92.9%; Pred. No. 6e+05; ive 0; Mismatches 1; Indels
                                                                                                    6; Length 17;
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An antisense oligonucleotide preparation method.
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Location/Qualifiers
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Best Local Similarity 92.9%; Pred. No. 6e+05;
Matches 13; Conservative 0; Mismatches
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synthetic construct
other sequences; artificial sequences.
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Sequence 2566 from Patent WO0129262.
AX117443
              /organism="Homo sapiens"
/mol_type="unassigned DNA"
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    .17
    /organism="unidentified"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 1512 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Patent: WO 03040369-A 5634 15-MAY-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03004526-A 1175 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX762313.1 GI:32256929
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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E 3 (bases 1 to 20)
E 4 (bases 1 to 20)
E 6 (bases 1 to 20)
E 7 (bases 1 to 20)
E 8 (connors, T.D., Burn, T.C. and Splawski, I.

CONNORS, T.D., Burn, T.C. and Splawski, I.

EVYLQTI-QT extension syndrome

L 8 Patent: JP 2003521045-A 77 16-UUL-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION, GENZYME CORP

OS Homo sapiens (human)
EN JP 2002521045-A 77
ED 16-UUL-2002
EP 12-MAY-1999 JP 200562052
EP 29-UUL-1999 US 60/094477, 17-AUG-1998 US 09/135010 FI

MARK T KEATING, MICHAEL C SANGUINETTI, MARK E KARAN, GREGORY M PI
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                                                           PAT 17-JUL-2003
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CI2N15/00,
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CL2N15/09, A01K67/027, C07K14/46, C07K14/47, C07K16/18, C12N1/15, PC
C12N1/19,
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Trofatter, J.A., MacCollin, M.M. and Gusella, J.F.
Tumor suppressor gene merlin
Patent: US 5707863-A 77 13-JAN-1998;
Location/Qualifiers
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Pred. No. 5.9e+05;
0; Mismatches 1;
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Key Location/Qualifiers
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Sequence 77 from patent US 5707863.
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    .20
    /organism="Homo sapiens"
/mol_type="genomic DNA"
    /db_xref="taxon:9606"

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KVLQT1-QT extension syndrome.
BD222879
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                                                                                                           BD222879.1 GI:33032649
JP 2002521045-A/77.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 92.9%;
Matches 13; Conservative
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Keating, M.T., Sanguinetti, M.C. and Splawski, I.
Mutations in the KCNEI gene encoding human minK which cause
arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
Patent: US 6274332-A 79 14-AUG-2001;
Location/Qualifiers
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Unclassified.
E 1 (bases 1 to 20)
E 1 rofatter, J. A., MacCollin, M.M. and Gusella, J.F.
Trofatter, J. A., MacCollin, M.M. and Gusella, J.F.
Tumor suppressor merlin and antibodies thereof
AL Patent: US 6077685-A 77 20-UN-2000;
Location/Qualifiers
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            /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noce="pximer"
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Sequence 79 from patent US 6274332.
AR164768.1 GI:16237937
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 77 from patent US 6077685.
AR098941.1 GI:12808707
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Matches 13; Conservative
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AR098941/c
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AR164768/c
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Tobases 1 to 20)

Keating, M.T., Sanguinetti, M.C. and Splawski, I.

Mutations in the KCNE1 gene encoding human mink which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene Patent: US 6323026-A 79 27-NOV-2001;

Location/Qualifiers
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    PAT 20-DEC-2002
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Keating, M.T., Sanguinetti, M.C., Curran, M.E., Landes, G.M.,
Connors, T.D., Burn, T.C. and Splawski, I.
Diagnostic method for KVLQT1--a long QT syndrome gene
Patent: US 6582913-A 79 24-JUN-2003;
                                                                                                              Unclassified.

1 (bases 1 to 20)

Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.

KVLQTI--a long QT syndrome gene

RVLQTI--a long QT syndrome yene
Patent: US 6451534-A 79 17-SEP-2002;
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Pred. No. 5.9e+05;
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AR344603
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Sequence 79 from patent US 6323026.
AR262165
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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92.9%;
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Best Local Similarity 92.9%;
Matches 13; Conservative
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AR344603/c
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AR262165/c
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1 (bases 1 to 20)

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Mutations in the KCNEI gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
Patent: US 6432644-A 79 13-AUG-2002;
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Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
KVLQT1--a long qt syndrome gene
Patent: US 6420124-A 79 16-JUL-2002;
Location/Qualifiers
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                                    62.0%; Score 12.4; DB 6; Length 20; 92.9%; Pred. No. 5.9e+05; ive 0; Mismatches 1; Indels
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Sequence 79 from patent US 6432644.
AR223147
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/mol_type="genomic DNA"
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AR218732.1 GI:23319627
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Best Local Similarity 92.9'
                                                                      13; Conservative
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Herrnstadt, C. and Davis, R.E. Single nucleotide polymorphisms in mitochondrial genes that segreg are with alzheimer's disease Patent: WO 0063441-A 166 26-OCT-2000; MITOKOR (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/or_l_type="unassigned DNA"
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/note="Cdk-we-hu ribozyme binding site"
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82.4%; Pred. No. 7.5e+05;
vative 0; Mismatches 3;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
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synthetic construct
other sequences; artificial sequences.
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Sequence 166 from Patent WO0063441.
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192224-A 8114 06-DEC-2001;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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                                                                                             ch 62.0%; Score 12.4; DB 6; Length 20; 1 Similarity 92.9%; Pred. No. 5.9e+05; 13; Conservative 0; Mismatches 1; Indels
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Sequence 8114 from Patent W00192524.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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    /organism="unknown"
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1/ DD DNA linear PAT 17-JUL-2003
Regulation of repressor genes using nucleic acid molecules.
BD259354
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PN JP 2002541795-A/7147
PD 10-DEC-2002
PP 11-APR-1999 US 60/129390
PI LAPR-1999 WS 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN
C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12NS/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Pegulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 7147 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
                                                                                  (Dases 1 to 20)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallellic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 8500 25-MAR-2003;
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/db_xref="taxon:32644"
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    /organism="unknown"

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 GI:31684049
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                                                                                                                                                                                                        Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
                                                                                                                                                       Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%; Pred. No. 9.4e+05;
Conservative 0; Mismatches 0;
                            17 bp DNA
Sequence 3140 from Patent WO03004526.
AX674695
                                                                                                                                                                                                                                                                          Patent: WO 03004526-A 3140 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03025175-A 397 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 8500 from patent US 6537751.
AR296765
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Sequence 397 from Patent WO03025175.
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
                                                                                     AX674695.1 GI:29333043
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Homo sapiens
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nes 12; Conserva
                                                                                                                                         Homo sapiens
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AR296765/c
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                                                   DEFINITION
                                                                   ACCESSION
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RESULT 26
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
              2
                                           (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC
C12P21/02,C12P21/02/A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, i
C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules l
Key
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 91 16-AUG-2001;
RIBOZYME HARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 1.2e+06;
0; Mismatches 2;
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86.7%; Pred. No. 1.2e+06;
tive 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db xref="taxon:32630"
/noTe="Nucleic Acid"
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Sequence 92 from Patent WO0159103.
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    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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PN JP 2002541795-A/7149
PN 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PR 12-APR-1999 US 60/129390
CL2N15/09, A61K38/00, A61K48/00, A61P43/00, CL2N5/10, PC C12P21/02,
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Bregulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 7149 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
                                     HDZ59355 17 bp DNA linear PAT 17·
Regulation of repressor genes using nucleic acid molecules.
BDZ59355
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Sagnlation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 7148 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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86.7%; Pred. No. 1.2e+06;
iive 0; Mismatches 2;

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(C12N5/00,C12R1:91)
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JP 2002541795-A/7149.
                                                                                            BD259355.1 GI:33069125
JP 2002541795-A/7148.
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PC (C12P)
PC A61K3
PC A61K3
PC (C12N)
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BD259356
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: EP 1273560-A 226 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: BP 1273560-A 227 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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                                                                                  Score 11.8; DB 6;
Pred. No. 1.2e+06;
0; Mismatches 2;
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Sequence 227 from Patent EP1273660.
AX648387
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Sequence 226 from Patent BP1273660.
AX648386
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0159103-A 92 16-AUG-2001;
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Human sodium-hydrogen exchanger like protein 1
Patent: EP 1273660-A 225 08-JAN-2003;
Aeomica, Inc. (US)
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Sequence 1738 from Patent WO0129262.
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AXII6615.1 GI:14033557
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Sequence 1 from patent US 5851769.
AR067594 AR067594.1 GI:5998816
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15 TCATGCAAGAAGCGG 1
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4 US-09-866-108A-6216 4 US-09-866-108A-6217 4 US-09-866-108A-6218 4 US-09-866-108A-6219	2 US-09-256-496-3 US-09-517-584A	3 US-09-658-687A 4 US-09-198-452A 4 US-09-856-662-4 1 US-09-856-662-3	4 US-09-476-387- 4 US-09-866-108A 4 US-09-866-108A 4 US-09-866-108A	4 US-09-866-108A 4 US-09-696-791-	1 US-07-128-363 1 US-07-977-284A 2 US-08-256-426B	4 US-09-954-560- 4 US-10-029-517-	4 US-09-232-785- 1 US-08-311-760A 1 US-08-311-760A	2 US-08-774-310- 2 US-08-774-310-	4 US-09-474-4325 4 US-09-476-387- 3 HS-08-985-162-	3 US-08-985-162- 4 US-09-474-432B	4 US-09-371-772B 4 US-09-476-387-	4 US-09-401-063- 4 US-09-401-063- 4 HS-09-866-108A	4 US-09-866-108A	4 US-09-866-108A 4 US-09-877-177A	4 US-09-663-834A 3 US-09-676-610B	4 US-09-696-791-	2 US-08-809-297-	3 US-09-487-368A	3 US-09-702-251-	4 US-09-629-644A	4 US-09-595-684B 4 US-09-198-452A	4 US-09-629-644A 4 US-10-177-573-	3 US-08-679-645-	4 US-09-866-108A	4 US-09-866-108A 3 US-09-161-244-	4 US-09-747-391-	1 US-08-157-235-	1 US-08-832-172-	2 US-08-470-426B	2 US-U8-53/-923- 3 US-09-167-921-	3 US-08-647-924- 3 US-09-323-743- 4 US-09-216-393E	
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	nucleic search, using sw model	Secor ents) cell	US-10-773-678-342 20 1 gactcttgcaggaagcggct 20	IDENTITY NUC Gapop 10.0 , Gapext 1.0	1202784 seqs, 818138359 residues		ength: 0 ength: 20		Listing first 100 summaries	£	<pre>2: /cgiiz_b/ptodata(1/ina//b-com:seq. 3: /cgn2_b/ptodata(1/ina/6A_COMB.seq.* 4: /cgn2_b/ptodata(1/ina/6B_COMB.seq.*</pre>		ted by chance to have a	ved by analysis of the total score distribution.	SUMMARIES	ery handthom ID Descripti		0 20 4 US-09-788-461-19 Sequence 19,	.0 20 4 US-09-081-365-134 Sequence 13-	.0 20 3 US-08-478-087-77 Sequence 77, 0 20 3 US-09-135-020-79 Sequence 79,	0 20 3 US-09-135-010A-79 Sequence 79	0 20 3 US-09-597-735-79 Sequence 79	.0 20 3 US-09-444-253-79 Sequence 79	.0 20 4 US-09-597-731-79 Sequence 79. .0 17 4 US-09-866-108A-8114 Sequence 81.	.0 19 4 US-09-696-791-1380 Sequence 130	.0 20 4 US-09-425-9/0-0500 Sequence of	.0 20 2 US-08-534-4/9-1 Sequence 1.	.0 20 4 US-09-596-248D-38 Sequence 38 .0 20 4 US-09-596-248D-39 Sequence 39	.0 20 4 US-09-972-115A-29 Sequence 29 .0 17 4 US-09-866-108A-115 Sequence 11:	.0 17 4 US-09-866-108A-116 Sequence 11.	Sequence 11 Sequence 11	.0 17 4 US-09-866-108A-6215 sequence 62

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Sequence 19, Application US/09758881

j Batent No. 6/27064

j Patent No. 6/27064

j Patent No. 6/27064

j Patent No. 6/27064

j Patent No. 6/27064

j TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

j TITLE OF INVENTION: Expression

f TITLE OF INVENTION: 2001-01

prior APPLICATION NUMBER: US/09/758,881

prior APPLICATION NUMBER: PCT/US00/09054

prior APPLICATION NUMBER: 09/288,461

prior APPLICATION NUMBER: 09/288,461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                      Sequence 19, Application US/09288461
; Betent No. 6159694
; GENERAL INFORMATION:
    APPLICANT: KARTAS, James G.
    TITLE OF INVENTION: Attisense Oligonucleotide Modulation of STAT3
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: BXDFSESSION
    CURRENT FILING DATE: 1999-04-08
    NUMBER OF SEQ ID NOS: 107
    SOFTHARE: PatentIn Ver. 2.0
    SEQ ID NO 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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100.0%; Pred. No. 9.3e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.0%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 9.3 Matches 14; Conservative 0; Mismatches
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic Sequence
US-09-288-461-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACTCTTGCAGGAA 14
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Matches 14; Conservative
                                                                                                                            US-09-288-461-19
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Sequence 134, Application US/09081385 Patent No. 6593456

RESULT 3 US-09-081-385-134

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Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity, and Methods
of Use Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 77, Application US/08171718

Patent No. 5707863

GENERAL INFORMATION:
APPLICANT: Trefater, James A.
APPLICANT: MacCollin, Mia M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Thereof
ITILE OF INVENTION: Thereof
CORRESPONDENCE ADDRESS: 120
CORRESPONDENCE Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: D.C. COUNTY: USA ZIP: 20005-3334 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                        COMPUTRY: USA
ZIP: 94304-1018
COMPUTRY READABLE FORM:
MEDUTUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
CURRARET APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22000-20577.21
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-26
TELECOMMUNICATION INFORMATION:
TELECHNNE: 650-819-5600
                   APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Alterir
TITLE OF INVENTION: G. Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TCTTGCAGGAAGCGGC 19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
GENERAL INFORMATION:
APPLICANT: Gatana
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STRANDEDNESS:
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Sequence 79, Application US/09135020
Patent No. 6274332
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/135,020
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATCHILN Ver: 2.0
                                                                                                                                                                                         0609.3850003
                                                       PRIOR APPLICATION DAINS:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEY AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 06,463
REFERENCE/DOCKET NUMBER: 0609.385000
TELECHONICATION INFORMATION:
TELECHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDENNES: single
  US 08/022,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-135-010A-79/c
; Sequence 79, Application US/09135010A
; Satent No. 6277978
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.0%;
92.9%;
                        25-FEB-1993
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APPLICATION NUMBER: UFILING DATE: 25-FEB-1PRIOR APPLICATION DATA: APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-135-020-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 13; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-478-087-77
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US-09-135-020-79/c
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LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Trofatter, James A.
APPLICANT: MacCollin, Mia M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS: 220
CORRESPONDENCE ADDRESS: 320
CORRESPONDENCE ADDRESS: 400
CITY: Washington
STRATE: D.
COUNTRY: USA
COUNTRY: USA
ZIP: 20005-3934
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DATE OF COMPATA:
APPLICATION NUMBER: US/08/478,087
FILING DATE: 07-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/171,718
FILING DATE: 250
PRIOR APPLICATION NUMBER: US 08/171,718
FILING DATE: 250
FILING DATE: 19-AUG-1993
FILING DATE: 19-AUG-1993
FILING DATE: 19-AUG-1993
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Pred. No. 6e+03;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE PALICATION DATA:
APPLICATION NUMBER: US/08/171,718
FILING DATE: 22-DEC-1993
CLASSIFICATION: 436
                                                                                                                                                          PULBASIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIDIAG DATE: 19-AUG-1993
PRIDIAG DATE: 2-FEB-1993
FILING DATE: 2-FEB-1993
FILING DATE: 2-FEB-1993
FILING DATE: 2-FEB-1993
FILING DATE: 0-FEB-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 0-FEB-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 0-FEB-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 0-FEB-1993
APPLICATION NUMBER: US 06/09.3850003
FELEFONEY (202) 371-2600
TELEFONEY: (202) 371-2600
TELEFONE: (202) 371-2540
INPORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 77, Application US/08478087
Patent No. 6077685
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-171-718-77
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US-08-478-087-77/c
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APPLICANT: Sanguinetti, Michael C.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Splawski, 1gor

TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN minK WHICH

TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ESTABLISHING

TITLE OF INVENTION: KCNEI AS AN LQT GENE

FILE REPERENCE: 2123-131

CURRENT APPLICATION NUMBER: US/09/444,871

CURRENT FILING DATE: 1999-11-22

EARLIER PELING DATE: 1999-08-17

EARLIER FILING DATE: 1996-10-30

EARLIER PELING DATE: 1996-10-4

EARLIER PELING DATE: 1996-10-4

EARLIER PELING DATE: 1996-10-20

EARLIER PELING DATE: 1996-10-20

EARLIER PELING DATE: 1996-10-20

EARLIER PELING DATE: 1996-10-20

EARLIER PILING DATE: 1998-10-29

EARLIER PILING DATE: 1998-10-29

WUMBER OF SEQ ID NOS: 114

SOFTWARE: PARENT PARE
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APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Connors, Timothy M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Splawski, 120.
ITILE REFERENCE: 2323-133
FILE REFERENCE: 2323-133
FURRENT FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 06/094,477
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1996-07-29
FRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1996-10-29
FRIOR APPLICATION NUMBER: 08/739,383
FRIOR APPLICATION NUMBER: 08/739,383
FRIOR APPLICATION NUMBER: 06/019,014
FRIOR FILING DATE: 1996-10-29
FRIOR PELING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 79
FRIOR FILING DATE: 1995-12-22
INTHREE PATENTING DATE: 
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; Sequence 79, Application US/09444871
; Patent No. 6323026
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Best Local Similarity 92.99
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-444-871-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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HEADLICANT: CATALON WARKE TO A LONG OF SYNDROME GRNE
PREATE NO. 623124

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GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yongang

APPLICANT: PENN, Sharron G.

APPLICANT: RANK, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REPERENCE: AEOMICA-7
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-00-04
PRIOR PLILING DATE: 2000-00-07
PRIOR FILING DATE: 2000-00-07
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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6e+03;
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Pred. No. 6e+03
0; Mismatches
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CURRENT FILING DATE: 2001-05-25
                           PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR APPLICATION NUMBER: 1995-12-22
NUMBER OF SEQ ID NOS: 116
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2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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CRGANISM: Homo sapiens
US-09-597-731-79
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US-09-866-108A-8114
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SEQ ID NO 79
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Pred. No. 6e+03;
0; Mismatches 1; Indels
                                                                                                                                                                         Score 12.4; DB 3; Length 20;
Pred. No. 6e+03;
0; Mismatches 1; Indels
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PPLICANT: Splawski, Igor
ITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Keating, Mark T.
APPLICANT: Kaating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Blurn, Timothy C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KVLOT1 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE KEPEKENCE: 1232-1133
CURRENT PEDLICATION NUMBER: US/09/597,732
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-07-29
PRIOR PRILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-39
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PALENTIN VET: 2.0
SOFTWARE: PALENTIN VET: 2.0
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Patent No. 6451534
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Sanguinetti, Michael
Curran, Mark B.
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Connors, Timothy D.
Burn, Timothy C.
                                                                                                                                                                               62.0%;
92.9%;
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-732-79
                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-444-295-79
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APPLICANT: Keating,
APPLICANT: Sanguine
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APPLICANT:
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                                    LENGTH: 20
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      SEQ ID NO 79
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Sequence 130, Application US/09487445

Patent No. 6258600

GENERAL INFORMATION:
APPLICANT: Hong Zhomgert

TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION FILE REFERENCE: FTS-0107

CURRENT APPLICATION NUMBER: US/09/487,445

CURRENT FILING DATE: 2000-01-19

NUMBER OF SEQ ID NOS: 176

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%; Score 11.8; DB 3;
86.7%; Pred. No. 1.2e+04;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, KAMRIN T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: LBL-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 20 GACTTTTGCACTAAGCAGAT
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MOLECULE TYPE: DNA (genomic)
US-08-534-479-1
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                           RESULT 16
US-09-487-445-130/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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US-09-422-978-8500/c

Sequence 8500, Application US/09422978

Sequence 8500, Application US/09422978

Sequence 8500, Application US/09422978

Sequence 8500, Application US/09422978

SEMELER LINFORMATION:

APPLICANT: Chumakov, IJya

APPLICANT: Chumakov, IJya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REPERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/09/422, 978

CURRENT APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1999-04-21

EARLIER PILING DATE: 1999-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-11-23

SEQ ID NO 8500

LENGTH: 20

LENGTH: 20

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APPLICANT: Robbins, Joan M.

APPLICANT: Tritz, Richard

TITLE OF INVENTION: SKIN AND EYE DISEASES

TITLE OF INVENTION: SKIN AND EYE DISEASES

TITLE OF INVENTION: SKIN AND EYE DISEASES

TITLE OF INVENTION: OWNER: US/09/696,791

CURRENT APPLICATION NUMBER: US/09/696,791

CURRENT FILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4523

SEQ ID NOS: 4523

SEQ ID NO 1380

LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 12; DB 4; Length 20; 75.0%; Pred. No. 9.6e+03; tive 0; Mismatches 5; Indels
82.4%; Pred. No. 7.4e+03;
iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Cdk-we-hu ribozyme binding site US-09-696-791-1380
                                                                                                                                                                                                                                Sequence 1380, Application US/09696791
Patent No. 6770633
                                                                       4 TCTTGCAGGAAGCGGCT 20
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Best Local Similarity 75.0
Matches 15; Conservative
Best Local Similarity 82.4
Matches 14; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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US-09-696-791-1380/c
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ò g 1 GACTCTTGCAGGAAGCGGCT 20

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APPLICANT: Christenson, Brik
APPLICANT: Christenson, Anthony J
APPLICANT: DeMaggio, Anthony J
APPLICANT: DeMaggio, Anthony J
APPLICANT: Dedman, Phyllis S
APPLICANT: McElligott, David L
TITLE OF INVENTION: Methods
TITLE OF INVENTION WIMBER: US/09/596,248D
CURRENT APPLICATION NUMBER: US/09/596,248D
CURRENT FILING DATE: 1999-06-16
NUMBER: OF SEQ ID NOS: 68
SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.0%; Score 11.6; DB 4; Length 20; 77.8%; Pred. No. 1.5e+04; Live 0; Mismatches 4; Indel8
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APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 20
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Patent No. 6599728
GENERAL INFORMATION:
APPLICANT: Geron Corporation
                                                        ; Sequence 39, Application US/09596248D; Patent No. 6599727; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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Best Local Similarity
Matches 14; Conserv
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US-09-972-115A-29
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                                           US-09-596-248D-39
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LENGTH: 20
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Patent No. 6258351

GENERAL INFORMATION:
APPLICANT: Susan Murray
APPLICANT: Lex M. Cowsert
APPLICANT: Jacqueline Wyatt
TILE REFERENCE: RTS-0110
CURRENT APPLICATION NUMBER: US/09/489,869A
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 49
LENGTH: 20
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APPLICANT: Dewaggio, Anthony J
APPLICANT: Goldman, Phyllis S
APPLICANT: McElligott, David L
TITLE OF INVENTION: Human Poly(ADP-Ribose) Polymerase 2 Materials and
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
FILE REFERENCE: 27866/36544
CURRENT APPLICATION NUMBER: 105/09/596,248D
CURRENT FILING DATE: 2000-06-16
PRIOR PILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 68
SEQ ID NOS: 68
SEQ ID NO 38
LENGTH: 20
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Query Match 58.0%; Score 11.6; DB 2; Length 20; Best Local Similarity 77.8%; Pred. No. 1.5e+04; Matches 14; Conservative 0; Mismatches 4; Indels
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58.0%; Score 11.6; DB 3;
Best Local Similarity 77.8%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 4;
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. Sequence 38, Application US/09596248D
. Patent No. 6599727
; GENERAL INFORMATION:
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APPLICANT: DeMaggio, Anthony
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US-09-489-869-49/C
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: Homo sapiens
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APPLICANT:
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APPLICANT:
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APPLICANT: GU, YiZhong
APPLICANT: GU, YiZhong
APPLICANT: DI, YiZhong
APPLICANT: PERN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                           THE KEEKERENCE: ABCONICATION NUMBER: US/09/866,108A
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-010-04
PRIOR PELING DATE: 2000-010-04
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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                         Sequence 115, Application US/09866108A Patent No. 6686188
                                                                                                GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                            RANK, David R. CHEN, Wensheng
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US-09-866-108A-116
US-09-866-108A-115
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APPLICANT:
APPLICANT:
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US-09-866-108A-119
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 118
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARB: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 117
LENGTH: 17
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                                                                                                                                                                                                                                                   Length 17;
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Pred. No. 1.9e+04;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: GB 24263.6
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 118, Application US/09866108A Patent No. 6686188 GENERAL INFORMATION:
APPLICANT: GU, Yizhong APPLICANT: JI, Yonggang
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-118
                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-866-108A-117
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APPLICANT: CHIN, Wensheng
APPLICANT: CHIN, Wensheng
APPLICANT: CHIN, WASIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
ITILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 20
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
IIILE OF INVENTION: MYSOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
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Pred. No. 1.9e+04;
0; Mismatches 1;
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209-86-108A-6215/c
; Sequence 6215, Application US/09866108A
; Patent No. 6686188
Sequence 119, Application US/09866108A Patent No. 6686188
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92.3%;
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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APPLICANT: SHANNOW, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-00-26
PRIOR PELING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
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Pred. No. 1.9e+04;
0; Mismatches 1;
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                                                                                                                  SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 6216
LENGTH: 17
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; Sequence 6217, Application US/09866108A
; Patent No. 6686188
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92.3%;
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PRANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
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Best Local Similarity 92.3
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108A-6217
                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo s
US-09-866-108A-6216
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEGMICA-7
FILE REFERENCE: AEGMICA-7
CURRENT PAPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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US-09-866-108A-6216/c
US-09-866-108A-6216/c
Sequence 6216, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: Ul. Yanggang
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
                      FILING DATE: 2000-05-26
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
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Best Local Similarity 92.3
Matches 12; Conservative
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ORGANISM: Homo sapiens
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US 60/207, 456
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Best Local Similarity
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; ORGANISM: Homo 8
US-09-866-108A-6219
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US-09-866-108A-6219/C
; Sequence 6219, Application US/09866108A
; Patent No. 666618B
; GENERAL INFORMATION:
; APPLICANT: UI, Yizhong
; APPLICANT: PENN, Sharron G.
; APPLICANT: RANK, David K.
; APPLICANT: RANK, David K.
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7;
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-10-26

PRIOR FILING DATE: 2000-10-04-27

PRIOR PLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2001-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/US01/00664

PRIOR PLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PR
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Wark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
                                                                                                                                               Sequence 6218, Application US/09866108A
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Best Local Similarity 92.3%;
Matches 12; Conservative (
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GI, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEARN. COWSERT
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION
TITLE OF INVENTION: MUNBER: US/09/256,496
CURRENT APPLICATION UNBER: US/09/256,496
CURRENT FILING DATE: 1999-02-23
SEQ ID NO 10
LENGTH: 18
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Pred. No. 1.9e+04;
); Mismatches 1;
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Pred. No. 1.9e+04;
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Patent No. 6686188
SEQ ID NO 6219
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US-09-517-584A-11/c
; Sequence 11, Application US/09517584A
; Patent No. 618750';
GENERAL INFORMATION:
; APPLICANT:
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; Sequence 10, Application US/09256496
; Patent No. 5998206
; GENERAL INFORMATION:
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92.3%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 92.3
Matches 12; Conservative
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Sequence 6247, Application US/09198452A

Patent No. 6559294

GRNERAL INFORMATION:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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Sequence 20, Application US/09856662

GENERAL INFORMATION:
APPLICANT: MORIBE, TOYOKi et al.
TITLE OF INVENTION: Method for typing HLA class 1 genes
FILE REFERENCE: 0032-0261P
CURRENT APPLICATION NUMBER: US/09/856,662

CURRENT FILING DATE: 2001-05-24

PRIOR FILING DATE: 1998-11-26

NUMBER OF SEQ ID NOS: 130

SEQ ID NO 20

LENGTH: 16
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                                                                                                             Pred. No. 1.9e+04;
                                                                                                                             0; Mismatches
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; Patent No. 6528640
; GENERAL INFORMATION:
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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6247
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                                                                                                             92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                            Best Local Similarity 92.3
Matches 12; Conservative
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US-09-474-432B-429
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us-10-773-6

APPLICANT: Vickie L. Brown-Driver
APPLICANT: Lex M. Cowsert
ITLE OF INVENTION: RTS-0121
CURRENT APPLICATION NUMBER: US/09/517,584A
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 11
LENGTH: 20
TYPE: 20
TYPE: 20
TYPE: 20
TYPE: 20
TYPE: 20
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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
FILE REFERENCE: RTS-0088
CURRENT APPLICATION NUMBER: US/09/467,082
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 27
LENGTH: 20
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Sequence 51, Application US/09658687A

Patent No. 6387699

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

TILE OF INVENTION: ANYSENSE MODULATION OF A20 EXPRESSION

TILE REFERENCE: RTS-0141

CURRENT APPLICATION: NUMBER: US/09/658,687A

CURRENT FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 88

SEQ ID NO 51

LENGTH: 20
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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Pred. No. 1.9e+04;
0; Mismatches 1;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-51
                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Antisense Oligonucleotide US-09-517-584A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 27, Application US/09467082; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.0%;
Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3%;
Matches 12; Conservative
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GENERAL INFORMATION:
APPLICANT: GI, Yichong
APPLICANT: GI, Yougang
APPLICANT: GI, Yougang
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HANK, David R.
APPLICANT: HANK, David R.
APPLICANT: GIANK, David R.
APPLICANT: GIANNON, MARK
ITITE OF INVENTION: MYNGER: US/09/866,108A
CURRENT PLING DATE: 2001-05-25
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2001-0-04
PRIOR PLING DATE: 2001-0-10-04
PRIOR PLING DATE: 2001-0-10-04
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR DATE PRIOR DATE: 20
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Pred. No. 2.4e+04;
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                                                                                                                                                                              US-09-866-108A-7632/c
; Sequence 7632, Application US/09866108A
; Patent No. 6686188
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81.2%;
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Best Local Similarity 81.2
Marches 13, Conservative
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US-09-866-108A-7632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REPERENCE: MBH8100-831-8 (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
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Pred. No. 2.4e+04;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.0%; Score 11.2; DB 4; Length 17; Best Local Similarity 68.8%; Pred. No. 2.4e+04; Matches 11; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR FILING DATE: 1997-11-05
PRIOR FILING DATE: 1998-04-29
PRIOR PLILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1999-11-04
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PATCHIN VETSION 3.0
SEQ ID NO 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR PILING DATE: 1999-04-28
PRIOR FILING DATE: 1998-10-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-11-04
PRIOR PELING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 1524
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68.8%;
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Best Local Similarity 68.8
Matches 11; Conservative
Beigelman, Leo
                                Burgin, Alex
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US-09-474-432B-429
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Sequence:

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Adg14241 Human PLA
Adh3328 Human gen
Adh3328 Human gen
Adr4133 Human rhe
Aaf57367 Human rhe
Abn00127 Human GDM
Abn06228 Human GDM
Abn06229 Human GDM
Abn00123 Human GDM
Abn00128 Human GDM
Abn00128 Human GDM
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Abn00129 Human GDM
Abn002301 Human GDM
Acn69315 Human GDM
Acn69317 Human GDM
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Aah58956 Cdk-we-hu
Adt01798 Novel mut
Aat89003 Human mas
Aaz02042 PCR prime
Aax79782 PCR prime
Acx70917 Human cyt
Adm14320 Human mPG
Adm14505 Human mPG
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ACN63213
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ACN63216
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ADK95770
AAC66842
AAH42162
AAH23229
AAH20590
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ADD 25073
ABZ 99166
ABD 32197
ADK 95604
ABN08122
ACN71212
AAC 67455
AAA 667455
AAA 68956
ADT 01798
AAC 8003
AAC 800
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ADM14505
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ABT34760
ACC54373
ADF87984
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Aaf46590 IGFBP3 01
Aaf46589 IGFBP3 01
Aaf4658 Human mPG
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Aat90721 Human KVL
Aat91069 Human KVL
Aaz90745 Human KVL
Aaz98975 Mutant hu
Adr72365 Antisense
Adr72397 Antisense
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Aah39770 SNP speci
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                                                                                                                                  2005, 09:48:11; Search time 231 Seconds (without alignments) 512.532 Million cell updates/sec
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                         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Listing first 100 summaries
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ADE34379
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AAT90721
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AAZ98975
ADR72365
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ACC52408
                                                                                                   nucleic search, using sw model
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AAF46589
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AAS96785
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Gapop 10.0 , Gapext 1.0
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geneseqn2001as:*
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Match Length
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length: 20
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Minimum DB & Maximum DB #

Database

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Searched:

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Homo
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nucleobases in length, that is targeted to a nucleic acid molecule
encoding STAT3 (Signal Transducer and Activator of Transcription) and
which inhibits the expression of it. (1) has antinflammatory,
antirheumatic, cytostatic and immunostimulatory activities. (1) is used
for inhibiting the expression of STAT3 in cells or tissues, treating an
animal having a disease or condition associated with STAT3 or a human
chaving a disease or condition characterised by a reduction in apoptosis,
and inducing apoptosis in a cell. Diseases or conditions that are treated
and/or neck, leukaemia, myelonma, melanoma or lymphoma. (1) can also be
used for diagnostic methods in detecting and determining the role of
STAT3 in various cell functions, physiological processes and conditions
and for diagnostic the orditions associated with expression of STAT3:
(1) can be used alone or with other drugs as an immunostimulator. (1) is
used in sandwich and colourimetric assays, involving enzyme conjugation
and radiolabeling and is used in diagnostic kits. AAC93150 encodes human
STAT3 and AAC93231 encodes mouse STAT3 as given in the exemplification of
the present invention. AAC93151 to AAC93120 to AAC93231 to AAC932310 to AAC9323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense compound for inhibiting the expression of signal transducer and activator of transcription 3 (STAT3) in cells or tissues and treating diseases or condition associated with STAT3, such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention. AAC93151 to AAC93230 and AAC93232 to AAC93299 represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93300 represents a mismatch control oligonucleotide which are used in example
 Acn69314 Human GDM
Acn63214 Human GDM
                              Aaz57670 Human G-a
Aax96921 PCR prime
                                                              Aac72420 Single nu
Aaa54448 Primer fo
Aaf91296 Human E2F
                                                                                                                                                                                                                                                                                                                                                       Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide; modulation; signal transducer and activator of transcription; DNA-binding protein; signal transduction; inhibition; apoptosis; inflammatory disease; cancer; antiinflammatory; antirheumatic; cytostatic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma; melanoma; lymphoma; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                            Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:19.
                                                                                                                                                ALIGNMENTS
ACN69314
ACN63214
AAZ57670
AAX96921
AAC72420
AAA54448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 46; 104pp; English.
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 113244
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The invention relates to antisense compounds targeted to a nucleic acid molecule encoding a signal transducer and activator of transcription (STAT) protein, specifically STAT3, where the antisense compounds inhibit the expression of STAT3. The antisense sequences are useful for inhibiting the expression of STAT3 in cells or tissues, inducing Fasnediated apoptosis in cells, and sensitising cells to apoptosis. They are associated with STAT3. These disorders include inflammatory or autoimmune disease, particularly rheumatoid arthritis, cancers, such as those of the breast, prostate, brain and head and neck and leukaemias, myelomas, melanomas and lymphomas. Also treatable are human diseases or conditions characterised by a reduction in apoptosis or an insensitivity to apoptotic signals. The sequences of the invention can be used in clinical apoptotic signals. The sequences of the invention can be used in clinical
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAT3; human; signal transducer and activator of transcription; ss; STAT; antisense gene therapy; Fas-mediated apoptosis; inflammatory disease; autoimmune disease; trenuatoid arthritis; cancer; breast; prostate; head; neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis; antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         research, for detecting and determining the role of STAT3 in various cell functions and physiological processes and for diagnosing conditions associated with the expression of STAT3. The sequences represent cDNA encoding human STAT3 and human STAT3 oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antisense compound useful for treating and diagnosing inflammatory diseases and cancers, is targeted to a nucleic acid molecule encoding signal transducer and activator of transcription proteins.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human STAT3 antisense phosphorothioate oligodeoxynucleotide #18.
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                                                                                                                                Length 20;
                                                                                                                                                                                                  0; Indels
                                                                 Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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Pred. No. 5.5e+03;
                                                                                                                                                                                                     Mismatches
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100.0%; Fi
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06-APR-2000; 2000WO-US009054.
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from the present invention
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                                                                                                                                                                   Similarity
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                                                                     Query Match
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Example 7; Page 44; 201pp; English.
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                                                                                                                                                                                                                          1 GACTCTTGCAGGAAGCGGCT 20
                                                                                                                                                                                                                                             GATTCCTGCACGAAGTGGCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2000; 2000WO-AU000693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0140345P.
                                                                                                                                                                                                                                                                                                    AAF46591 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                 IGFBP3 oligonucleotide #11.
                                                                                                                                                                                                                                                                                                                                              30-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wraight CJ, Werther GA,
                                                                                                                                                                                                      16; Conservative
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                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200078341-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000.
                                                                                                                                                                                                                                                                                                                         AAF46591;
                                                                                                                                                                                                                                               20
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                RESULT 4
AAF46591/c
                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                              chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; introcommonal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunoomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nutripric; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prosteglandin E2 synthese (mpcSES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
                                                                                                                                                                                            Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1012.
                                ;
 Score 14; DB 6; Length 20;
Pred. No. 5.56+03;
    70.0%; bcc.
100.0%; Pred. No. -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "2'-O-methocyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 1012; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-2003; 2003WO-US030374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2002; 2002US-0413549P.
                                                    1 GACTCTTGCAGGAA 14
                                                                                                                              ADM14825 standard; DNA; 20
                                                                        7 cácrcrrccaccad 20
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                                                                                                                                                                        (first entry)
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                      Local Similarity 100.
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHAA ) PHARMACIA CORP.
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                                                                                                                                                                                                                                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                        modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_base
                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                        01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gierse JK;
                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                   ADM14825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ischemia.
             Query Match
                                                                                                                    ADM14825/c
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                                Matches
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c having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal chaving a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antishebetic, immunomodulator; cardiant, neuroprotective, antishabetic, immunomodulatory and cardiovascular activities, and can cophen meed for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 13.6; DB 12; Length 20; 80.0%; Pred. No. 8.6e+03; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edmondson SR;
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ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                         65.0%; Score 13; DB 4; Length 15; 100.0%; Pred. No. 1.7e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                         Sequence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edmondson SR;
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAF46590 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                            8 GCAGGAAGCGGCT 20
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                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                                                                                                           GCAGGAAGCGGCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-041421/05.
                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                            Matches
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     8888888888888
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-IRA Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectides which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperacovascular condition; hyperplasia; kidney disease; neoplaric of the retina; ss.
            neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                 ö
                                                                                                                                                                      65.0%; Score 13; DB 4; Length 15; 100.0%; Pred. No. 1.7e+04; tive 0; Mismatches 0; Indels
                                                                                                                                   Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                AAF46589 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGFBP3 oligonucleotide #9.
                                                                                                                                                                                                                                                      8 GCAGGAAGCGGCT 20
                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                               GCAGGAAGCGGCT 2
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                                                                                                                                                                          Query Match
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WPI; 2004-305094/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM14384;
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ADM14384/c
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                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic cancer; diagnosis; pancreatic cancer-associated gene; cytostatic; vaccine; gene therapy; human; reverse transcription; PCR; primer; 88; semi-quantitative RT-PCR experiment.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing pancreatic cancer (PNC) comprises determining a level of expression of a PNC-associated gene in a patient derived biological
disease, kidney disease, hyperproliferation of the inside of blood
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                                                                                                                                                                                                                                                                                                                                                                                 Pancreatic cancer related RT-PCR forward primer SEQ ID NO:13.
                                                                              Query Match 65.0%; Score 13; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 1.7e+04; Matches 13; Conservative 0; Mismatches 0; Indels
                                                  Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 13; 152pp; English
                   vessels or any other hyperplasia
                                                                                                                                                                                                                                                                             ADM92376 standard; DNA; 20 BP.
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28-FEB-2003; 2003US-0450889P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ONCO-) ONCOTHERAPY SCI INC. (UYTY ) UNIV TOKYO.
                                                                                                                                                                                                                                                                                                                                               01-JUL-2004 (first entry)
                                                                                                                                                      8 GCAGGAAGCGGCT 20
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Synthetic.
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ingredient and a pharmaceutical carrier; and (7) a method of predicting recurrence of PNC. The compounds have cytostatic activity, and can be used in vaccines and in gene therapy. The method is useful in diagnosing PNC or a predisposition to developing PNC in a subject. The methods, compounds and compositions are useful in treating or preventing PNC. The polypeptides are useful as vaccines against PNC. The present sequence represents a reverse transcription (RT) PCR primer used in semi-appresents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/note = "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.6; DB 12; Length 20; Pred. No. 2.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    used in an example from the present invention.
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/note= "2'-O-methocyethyls"
16. 20
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%;
78.9%;
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Best Local Similarity 78.99
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
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                                                                                                                                                                                                                                                                                                                                                                             antidiabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mores. Inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                          The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9d34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibite its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense compounds have cytostatic, antisense compounds have cytostatic,
               New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
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/note= "2'-0-methocyethyls"
                                                                                                                         Claim 4; SEQ ID NO 571; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.0
Best Local Similarity 78.9
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16. .20
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Synthetic.
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                                                                                   ischemia.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to organize the present invention also describes: (1) antisense compounds, paying a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically phybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mpGES-1. MpGES-1 chimeric antidiabletic, immunomodulator, cardiant, neuroprotective, cantidiabletic, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mpGES-1 e.g., inflammation, Alzheimer's condition associated with mpGES-1 e.g., inflammation, Alzheimer's chisease, arthritis, diabates, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                   New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 12.6; DB 12, 78.9%; Pred. No. 2.6e+04; tive 0; Mismatches 4,
/mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 1013; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ACTUTTGCAGGAAGCGGCT 20
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                                                                                                                              25-SEP-2003; 2003WO-US030374
                                                                                                                                                                     25-SEP-2002; 2002US-0413549P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 78.9
tes 15, Conservative
                                                                                                                                                                                                          (PHAA ) PHARMACIA CORP
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                                                                                             08-APR-2004.
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                                                                                                                                                                                                                                               Gierse JK;
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                                                                                                                                                                                                                                                                                                                                                                               ischemia.
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ADB45311
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WPI; 2001-290930/30
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAH39770;
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                                                                                                                                                                                                    fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombnant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis also be used to soreen for their specific interactive molecules.

Cond/or prognosis of these diseases. The nucleotides and polypeptides can also be used to soreen for their apsociated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                  New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
tumour regression; apoptosis; virus resistance; diagnosis;
cellular degeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
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Pred. No. 3.3e+04;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour suppressor sequence #1175.
                                                                                                                                                                                     Disclosure; Page 690; 771pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                   expression of the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC52408 standard; DNA; 17 BP.
                                                                    (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative C
                      17-SEP-2002; 2002WO-IB004219.
                                             17-SEP-2001; 2001FR-00011981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TCTTGCAGGAAGCG 17
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                                                                                          Amson R,
                                                                                                                WPI; 2003-441574/41.
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                                                                                          Telerman A,
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 15-MAY-2003
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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch.Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyxia; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                       regression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                         New nucleic acid sequences associated with tumor suppression, regressapprosts or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
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                                                                                     Tuijnder M, Telerman A, Amson R;
(MOLE-) MOLECULAR ENGINES LAB SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 311; 798pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 63; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH39770 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0160096P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TGCAGGAAGCGGCT 20
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circa of single musicalize purymosphisms ones. The presence of a SNP, using the coliqueds kits for determining the presence or absence of a SNP, using the coliqued strain for determining the presence or absence of a SNP, using the coliqued of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or classess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also includes appropent is or may be genetic such as autoimmune diseases of which a component is or may be genetic such as autoimmune cliesases, including, rheumatoid arthritis, multiple sclerosis, cancer, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and patematicy, according DNA sequence represents a PCR primer specific for a human SNP containing DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inspecting genetic susceptibility of Helicobacter pylori- related gastric carcinoma by checking Lewis blood-type antigen-associated gene polymorphism, applicable in screening individuals with high risk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori; gastric carcinoma; Lewis antigen; polymorphism; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for inspecting the genetic susceptibility of Helicobacter pylori related gastric carcinoma. The method of the invention comprises checking the polymorphism of the Le blood-type antigen-associated gene, with susceptibility particularly based on the recessive se allele and/or dominant homozygous Se/Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
single nucleotide polymorphisms SNPs. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.0%; Score 12.4; DB 4; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYPE-) UNIV PEKING SCHOOL ONCOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 14; 37pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ke Y, Jiang J, Ning T, Lu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE34379 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CTTGCAGGAAGCGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
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Matches 13; Conserv
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Lewis

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The sequences given in AAQ71110-55 are primers which were used to amplify the 17 exons of the NPZ gene. NPZ is a neurofibromatosis which is characterised by bi-lateral schwannomas. The NPZ "gene" has been shown by linkage studies to be assigned to chromosome 22. The missing or mutated gene in NPZ patients has been shown to be the merlin gene. The gene encodes a protein, merlin (moesin-ezin-radixin-like protein), which possesses tumour suppressor activity, and whose tumour suppressor activity, and whose tumour suppressor activity and whose tumour suppressor activity is mediated by interactions with the cytoskeleton. The merlin D22528. In patients suffering from NPZ, the merlin gene is either lost or mutated. A mutant merlin protein may be encoded by a gene in which a
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genotype. The method is applicable in screening individuals with high risk and in a follow-up survey for intervention, prevention and early diagnosis. In an experiment from the invention the Lewis gene fragments with TS9G, G508A and T1067A polymorphism sites for PCR amplification were obtained for use after extracting samples of peripheral lymphocyte DNA from subjects. The mutation was then identified for assessing disease risk and diagnosis. The current sequene represents a PCR primer for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma; sequence-tagged site assay; chromosome 22; NP2; deletion; hearing loss; neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D2S28; tumour suppressor; activity; meningioma; cytoskeleton; gene therapy; merlin-associated tumour; D2S28; posterior capsular lens opacity; deafness; balance disorder; paralysis; ss.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The tumour suppressor gene merlin - for treatment and diagnosis of tumours and neurofibromatosis (NF2).
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                                                                                                                                                                                                             Length 18;
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                                                                                                                                                                                                           62.0%; Score 12.4; DB 12; 92.9%; Pred. No. 3.3e+04; ative 0; Mismatches 1;
                                                                                                                                                                        Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                        amplification of a region of the Lewis gene.
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93US-00026063.
93US-00108808.
93US-00171718.
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ71136 standard; cDNA; 20
                                                                                                                                                                                                                                                                                      2 ACTCTTGCAGGAAG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                        ACTCTGGCAGGAAG 16
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                                                                                                                                                                                                                              Local Similarry
nes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1994;
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20-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ71136;
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syndrome; arrhythmia; minK; potassium channel; diagnosis;

us-10-773-678-342.max.rng

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Human KVLQT1 S4 region PCR primer 5.
                                                                                                                                                 KVLQT1; long QT syndrome; arrhy!
therapy; human; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                         (UTAH ) UNIV UTAH RES FOUND.
(GENZ ) GENZYME GENETICS.
                                                 AAT91069 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                               Keating MF, Curran ME,
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-402191/37.
                                                                                                                                                                                                                            WO9723632-A1.
                                                                                                                                                                                                     Homo sapiens
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                                                                                                  01-MAR-1998
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                                                                                                                                                                                        Synthetic
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                                                                          AAT91069;
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                                     AAT91069/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer 5 (AAT90721) and primer 6 (AAT90722) were designed to amplify DNA encoding the S4 region of human KVLQT1 (see AAW10038). PCR primers (AAT90717-28) were used in single-strand conformation analysis (SSCP) to define mutations in the human KVLQT1 gene (see AAT90710) associated with long QT syndrome (LQT). An initial SSCP identified an anomalous conformer in LQT-affected members of 6 large families. Further SSCP analyses identified a KVLQT1 intragenic deletion and 9 missense mutations associated with LQT in small families and sporadic cases
mutation of A to T at the first position of the codon encoding amino acid 220 causes the substitution of Tyr for Asn. The merlin gene may be used in gene therapy for the treatment of a merlin-associated tumour or NF2, or for prevention of schwarnoma, meningioma, posterior capsular lens opacities, deafness or hearing loss, balance disorders or paralysis.
                                                                                                                                                                                                                                                                                                                                                       KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel; diagnosis; therapy; human; single strand conformation polymorphism; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human minK and Xenopus KVLQT1 coding sequences – used for assays for identifying drugs which can be used for preventing or treating long \mathbb{Q}\mathbb{T}
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                                                                                                                                       Gaps
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                                                                                                            Score 12.4; DB 2; Length 20;
Pred. No. 3.3e+04;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                       Seguence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                              (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curran ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; Page 44; 105pp; English.
                                                                                                                                                                                                                                                                                                                                 Human KVLQT1 S4 region PCR primer 5.
                                                                                                                                                                                                                                                        AAT90721 standard; cDNA; 20 BP.
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                                                                                                                62.0%;
92.9%;
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hes 13; Conservative
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                                                                                                                                         13; Conservative
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                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                          12-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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Matches
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Matches
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Connors TD;

Landes GM,

95US-0019014P. 96WO-US019917.

96US-00739383

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                                                                                                                      PCR primer 5 (AAT91069) and primer 6 (AAT91070) were designed to amplify DNA encoding the S4 region of human KVLQT1 (see AAM33355). PCR primers (AAT91065-76) were used in single-estrand conformation analysis (SSCP) to define mutations in the human KVLQT1 gene (see AAT94004) associated with long QT syndrome (LQT). An initial SSCP identified an anomalous conformer in LQT-affected members of 6 large familites. Further SSCP analyses identified a KVLQT1 intragenic deletion and 9 missense mutations associated with LQT in small families and sporadic cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
New isolated human potassium channel gene, KVLQTI, - used to develop products for diagnosis, prevention and therapy of long QT syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                      62.0%; Score 12.4; DB 2; Length 20; 92.9%; Pred. No. 3.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human KVLQT1 mutation defining primer 5.
                                                                                Example 12; Page 44; 105pp; English.
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7 TGCAGGAAGCGGCT 20

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18 TGCAGGAAGCGGAT 5

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The invention relates to KVLQT1 nucleic acids which have a mutation compared to wild-type KVLQT1 (AAZ98901) The KVLQT1 gene encodes a protein of 676 amino acids which forms a cardiac I(ks) potessium channel with the KCNE1 protein (AAY80563). The KVLQT1 gene contains 15 introns and encodes a protein containing 6 putative transmembrane segments and a pore forming region. The gene has been mapped to the chromosomal location 11p15.5. The sequences AAZ98911-Z98982 represent PGR primers used to diagnose mutations in the KVLQT1 gene. Wutations in the KVLQT1 or KVNE1 genes result in cardiac arrhythmias observed as a prolonged QT curve in electrocardiograms (Long QT syndrome). The genes and proteins can be used for the diagnosis of subjects with long QT syndrome. They can also be used to screen for drugs which can be used for treating or preventing long QT syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER

/mod_base= OTHER= phosphorothioate nucleotide. All cytosines
are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are
2'-methoxyethyl nucleotides."
                                        New isolated mutant KVLQT1 nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; kinesin-like 1; NZ kinesin; bimC kinesin; cellular proliferation; cancer; B-cell leukaemia; autoimmune disease; carpal tunnel syndrome; Raynaud's phenomenon; systemic sclerosis; Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis; systemic lupus erythematosus; human; ss; ISIS 344901; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligo targeted to human kinesin-like 1, ISIS 344901.
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.0%; Score 12.4; DB 3; Length 20; Best Local Similarity 92.9%; Pred. No. 3.3e+04; Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          and KVLQT1 peptides can be used for peptide therapy
                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                           Example 13; Page 78; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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ADR72365 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TGCAGGAAGCGGCT 20
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             WPI; 2000-195199/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004180847-A1
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Rattus sp.
Synthetic.
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셤
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to KVLQT1 and KCNE1 genes, associated with long QT (LQT) syndrome. It provides a minK protein comprising a mutation which substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and treating LQT. The ability to predict LQT enables physicians to prevent the diseases with medical therapy such as beta blocking agents and opts for better treatments. Sequences AAZ90741-Z90752 represent PCR primers for defining human KVLQT1 mutations
                                                                                                                                                                                                                                                            Mutant forms of genes encoding minK protein and KVLQTI protein involved in cardiac potassium channel formation useful for screening drugs, for preventing and treating cardiac arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss;
cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
chromosome 11p15.5; PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant human long QT syndrome-associated KVLQT1 diagnostic primer 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.0%; Score 12.4; DB 3; Length 20; 92.9%; Pred. No. 3.3e+04; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                             Splawski I;
                                                                                                                                                                                                                                                                                                                            Example 13; Page 75; 167pp; English.
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Burn TC, Splawski I;
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                                                                                                                                                                                             Sanguinetti MC,
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Best Local Similarity 92.9
Matches 13; Conservative
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                WO200006600-A1
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17-AUG-1998;
                                                                               06-OCT-1998;
                                                                                                               29-JUL-1998;
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                                             10-FEB-2000
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Gaps

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The present invention relates to antisense compounds, compositions and methods for modulating the expression of kinesin-like 1. The superfamily of kinesins function as molecular engines to bind and transport vesticles and organelles along microtubules using energy supplied by ATP. Kinesin-like 1, a member of the N2 (also called bimC) family of kinesins, is involved in separating the chromosomes by directing their movement along microtubules in the bipolar spindle. Kinesin-like 1 is also known as KNSII, EGS, HEBGS, HKSP, KIFII, thyroid interacting protein 5 and TRIPS. Inhibition of kinesin-like 1 may be a target for arresting cellular of kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, arburitis, polymyositis and polyarteritis. Kinesin-like 1 is an autoantigen identified in systemic lupus erythematosus. The invention carburitis polymyositis and polyarteritis. Kinesin-like 1 is an autoantigen identified in systemic lupus erythematosus. The invention conding kinesin-like 1. Aleas provided are methods of screening for modulators of kinesin-like 1. Aleast a portion of the compound hybridises with RNA cto form an oligonucleotide-RNA duplex. It has at least one modified internucleoside linkage, sugar molety, or nucleobase. It has at least one cytosine which is a 5-methylcytosine. The antisense compound may comprise an antisense nucleic acid molecule that is specifically whybridisable with a 5'-untranslated region (UTR), with a start region, with a 3'-UTR, with an intron-ceron junction of a nucleic acid molecule encoding kinesin-like 1. ISI #344902.
                                                                                               New antisense compound 8 to 80 nucleobases in length targeted to a nucleic acid molecule encoding kinesin-like 1, useful for treating an animal having a disease or condition such as cancer, tumor, autoimmune
                                                                                                                                                                                                                                Example 30; SEQ ID NO 129; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinesin-like 1, ISIS #344902
Koller E;
                                                   WPI; 2004-652550/63
Dobie KW,
                                                                                                                                                                                    disease.
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62.0%; Score 12.4; DB 13; Length 20; 92.9%; Pred. No. 3.3e+04; tive 0; Mismatches 1; Indels 0 Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other; Best Local Similarity 92.8 Matches 13; Conservative Query Match

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Gaps

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a

ADR72397 standard; DNA; 20 ADR72397; ADR72397/

BP.

02-DEC-2004 (first entry)

Antisense oligo targeted to mouse kinesin-like 1, ISIS 285690.

Antisense; kinesin-like 1; N2 kinesin; bimC kinesin; cellular proliferation; cancer; B-cell leukaemia; autoimmune disease; carpal tunnel byndrome; Raynaud's phenomenon; systemic sclerosis; Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis; systemic lupus erythematosus; mouse; ss; human.

Mus musculus. Homo sapiens. Synthetic.

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cytosines
                          /noce= "OTHER= phosphorothioate nucleotide. All cytosine are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are 2'-methoxyethyl nucleotides."
                                                                                                                                                              New antisense compound 8 to 80 nucleobases in length targeted to a nucleic acid molecule encoding kinesin-like 1, useful for treating an animal having a disease or condition such as cancer, tumor, autoimmune
Location/Qualifiers
                     /mod base= OTHER
                                                                                  17-NOV-2003; 2003US-00714796
                                                                                                 23-MAY-2002; 2002US-00156603
               æ
        .. .20
*tag=
                                                                                                                                    Dobie KW, Koller E;
                                                                                                                                                   WPI; 2004-652550/63.
                                                                                                               (DOBI/) DOBIE K W.
                                                                                                                       (KOLL/) KOLLER E.
                                                        US2004180847-A1.
 Key
modified_base
                                                                      16-SEP-2004.
                                                                                                                                                                                      disease,
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Claim 36; SEQ ID NO 161; 110pp; English.

The present invention relates to antisense compounds, compositions and methods for modulating the expression of kinesin-like 1. The superfamily of kinesins function as molecular engines to bind and transport vesicles and organelles along microtubules using energy supplied by ATP. Kinesin-like 1, a member of the N2 (also called bind) family of kinesins, is involved in separating the chromosomes by directing their movement along microtubules in the bipolar spindle. Kinesin-like 1 is also known as KNSII, EgS, HRSP, KIFII, thyroid interacting protein 5 and TRIPS. Inhibition of kinesin-like 1 may be a target for arresting cellular proliferation in cancer, due to its central role in mitosis. Expression of kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, of kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, cof kinesin-like 1 expression may contribute to other disease states such autoantigen identified in systemic lupus erythematosus. The invention autoantigen identified in systemic lupus erythematosus. The invention correlates to antisense uncleic acid oligomers, targeted to the gene encoding kinesin-like 1. At least a portion of the compound hybridises with RNA cto form an oligonucleotide-RNA duplex. It has at least one modified internucleoside linkage, sugar moiety, prosphorothioate internucleoside linkage, sugar moiety, prosphorothioate internucleoside linkage, correlates and antisense nucleic acid molecule encoding kinesin-like 1.

Cromethoxyethyl sugar moiety, phosphorothioate internucleoside linkage, sugar moiety, or nucleobase. It has at least one cytosine which is a 5-methylcytosine. The antisense compound may comprise an antisense nucleic acid molecule encoding kinesin-like 1.

Cromethoxyethyl sugar moiety, phosphorothioate internucleoside linkage with a kinesin-like 1.

Gaps ö Score 12.4; DB 13; Length 20; Pred. No. 3.3e+04; 0; Mismatches 1; Indels Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other; 62.0%; 92.9%; 13; Conservative Local Similarity Query Match Matches

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TCTTGCAGGAAGCG 17 19 TCTTGCAGGAAGTG 6

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RESULT 21

Length 17;

61.0%;

ABN08122

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapy applement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart can skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence in this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO capture for the present sequence in the sequence
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                                                                                                                                                                                                                                                                                                                                      Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                             Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8114.
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ABN08122 standard; DNA; 17 BP
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30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
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30-JAN-2001, 2001WO-US000662.
30-JAN-2001, 2001WO-US000663.
30-JAN-2001, 2001WO-US000664.
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                                                                                                                                                                       (first entry)
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                             Human; ss; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                          Gaps
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0
Score 12.2; DB 6; Length 1
Pred. No. 4.1e+04;
0; Mismatches 3; Indels
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                                                                                                                                                                                                          Human GDMLP-1 probe SEQ ID NO:8114.
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
2001WO-US000661.
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2001WO-US000667.
2001WO-US000668.
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2001US-0266860P.
2001US-00866108.
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2001WO-US000665.
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               82.48;
                                                4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                  02-DEC-2004 (first entry)
  Query Match
Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENN S G.
HANZEL D K.
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CHEN W.
                                                                                                                                                                                                                                                                                                        US2004137589-A1.
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30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
05-FEB-2001; 2
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30-JAN-2001;
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(PENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GUXX/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HANZ/)
(RANK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHEN/)
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                                                                                                            RESULT 22
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AAA83794;
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                                                                                                                                                   Mammalia.
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                                                                                                                                                                                                                                                                                                   Tritz R,
  RESULT 24
               AAA83794/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH58956,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of or diagnosing Alzheimer's disease using single nucleotide polymorphisms (SNPs) present in an individual's mitochondrial DNA (mtDNA). In additon, the SNPs identified can be used to identify agents suitable for use in treating Alzheimer's disease. Sequences AAC67301-C67610 are PCR primers used to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a novel method for determining the risk
antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity hGDWLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing a subject at the risk for or having Alzheimer's disease comprises determining at least one single nucleotide polymorphism in mitochondrial DNA associated with the disease in the sample from the
                                                                                                                                                                                                                                                                                                                                                   Human; mitochondrial genome; single nucleotide polymorphism; SNP; Alzheimer's disease; mtDNA; PCR primer; ss.
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                            Alzheimer's disease-linked mitochondrial SNP PCR primer #155.
                                                                                                             61.0%; Score 12.2; DB 13; Length 17; llarity 82.4%; Pred. No. 4.1e+04; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
61.0%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                               invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 5 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                       Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 41; 89pp; English.
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                                                                                                                                                                                                                                                      ВР.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-2000; 2000WO-US010906
                                                                                                                                                                           TCCTGCCAGAAGCGGCT
                                                                                                                                                              4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                                                                                   AAC67455 standard; DNA; 18
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Davis RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-672748/65.
                                                                                                                        Local Similarity
es 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  WO200063441-A2.
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1999;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                      14-FEB-2001
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                                                                                                                                                                                                                                                                             AAC67455;
                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                             RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAAB415 to AAA86797. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                                                                   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.2; DB 3;
Pred. No. 4.1e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cdk-we-hu ribozyme binding site SEQ ID NO:1380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robbins JM;
                                                                                                                                                    cdk-we-hu ribozyme binding site #269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 67; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
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                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US028772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%;
82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ACTCTTGCAGGAAGCGG
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AAA83794 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2001 (first entry)
                                                                                                  04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                                      WO200032765-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998;
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2 ACTUTTGCAGGAAGCGG

17 ATTCTTGCACGAAACGG 1

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Vogelstein

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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for atti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FRS, GUCY2F and MCCK/MIX4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase stimulators. The invention may be useful for developing methods for detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a human-derived oligonucleotide
                                                                                                                                                                                                                                                                                                                                                 Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and associated methods for diagnosing cancer and screening for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maspin; serpin; mammary epithelial cell; human; promoter; malignant; tumour cell; treatment; prostate cancer; breast cancer; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.0%; Score 12.2; DB 13; Length 19; 82.4%; Pred. No. 4.1e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human maspin Ets wild-type sense oligonucleotide DNA.
                                                                                                                                                                                                                                                         Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1786; 363pp; English.
                                                                                                                                                                                                                                                            Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DAND ) DANA FARBER CANCER INST. (PARD/) PARDEE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT89003 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACTCTTGCAGGAAGCG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US005186.
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                                                                                          18-FEB-2004; 2004WO-US004452.
                                                                                                                                         21-FEB-2003; 2003US-0448537P.
29-MAY-2003; 2003US-0473895P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GACTGCTGCAGGAACG
                                                                                                                                                                                                             SNING ONIV JOHNS HOPKINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                              Parsons W,
                                                                                                                                                                                                                                                                                                          WPI; 2004-718702/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
WO2004082458-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                              Bardelli A,
                                            30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT89003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metaloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operably linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, christophalmological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, vulnerary, keratolytic and virucide activities, and clasves RNA encoding cytokine involved in inflammation. [1] can be used in gene therapy. [1] and [11] are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, aquamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detechment, and for treating and preventing prematurity and retinal detechment, and for treating and preventing carring such as keloid, adhesion and hypertrophic or hypertrophic burn sear.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine kinase; cancer; anti-cancer agent; signalling molecule; tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES; GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor; guanylate cyclase stimulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mutant protein tyrosine kinase-related oligonucleotide SeqID1786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 172; 408pp; English.
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82.4%;
                                                                                                                                                                                                                26-OCT-2000; 2000WO-US029500
                                                                                                                                                                                                                                                              99US-0161532P
  sickle cell retinopathy; ss
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nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                         Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                                                             (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-300427/31.
                                                                                                                   WO200130362-A2
                                              Homo sapiens
                                                                                                                                                                                                                                                                26-OCT-1999;
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                                                                                                                                                                   03-MAY-2001
                                                                         Synthetic
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                                                                                                                                        Query Match
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                                                                                                                                                            Matches
                                                                                                                                                                                                                                    RESULT 29
AAX79782/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivita; gential disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                experiments to analyse the maspin promoter region. AAT89003 is designed as a Ets regulatory element wild type (WT) sense oligonucleotide. Maspin is a serpin which is expressed in mammary epithelial cells. Its expression in these cells decreases with increasing malignancy and is lost in during metastasis. Maspin protein is also known to inhibit the mobility of tumour cells. This gene can be used in method for screening compounds to identify candidate compounds for the treatment of prostate cancer. It can also be used to identify compounds that increase the expression of maspin, and for detecting the presence of metastatic prostate epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
                                         Maspin gene promoter fragment - used to identify compounds for treatment of prostate or breast cancer.
                                                                                                         Primers AAT89003-T89008 are used in electrophoretic mobility shift assay
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                          Score 12.2; DB 2; Length 20;
Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                       Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 1492; 1755pp; English.
                                                                                    Disclosure; Page 12; 51pp; English
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97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                            Match 61.0%;
Local Similarity 82.4%;
les 14; Conservative
                                                                                                                                                                                                                                                                                                                           4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                                                                                                                                                                                                                AAZ02042 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-371125/31
                               WPI; 1997-489785/45
            Zhang M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09928475-A2
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04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                      AAZ02042;
            Sagar R,
                                                                                                                                                                                                                                                              Query Match
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                       against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, aslpingthis, perihepatitis, bartholinitis, pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
polypeptides (see AAY36754-Y37949) which can be used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic diagnosis using human mitochondrial DNA - comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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82.4%; Pred. No. 4.1e+04;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer H15340 for mitochondrial DNA analysis.
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82.4%; Pred. No. 4.1e
ive 0; Mismatches
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                               Gene detection method using human mitochondrial DNA to reveal and confirm amino acid substitution advantageous or disadvantageous in prolonged survival of human, useful for diagnosis of Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a detection method using human mitochondrial (mt) DNA. The method comprises detecting the replacement of a base accompanying an amino acid substitution in a protein encoded by its base sequence in a human mitochondrial DNA base sequence. The method is useful for diagnosis of Parkinson's disease, and in health checks and assessing risks for other adult diseases. The present sequence is a PCR primer, which was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; incrosomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nostropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation;
                                                                                                                                             Human; mitochondrial; Parkinson's disease; cytochrome b; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%; Score 12.2; DB 8; Length 20; 82.4%; Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                     (GIFU-) GIFU INT INST BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 35pp; Japanese.
                                                                                                                        Human cytochrome b PCR primer #10
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                                                              ВР
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                                                                                                                                                                                                                                                  17-OCT-2001; 2001JP-00318805
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ATTCTTGCACGAAACGG
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                                                             ACC70917 standard; DNA; 20
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                                                                                                      (first entry)
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                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-2004
                                                                                                      20-NOV-2003
                                                                                                                                                                                                          24-APR-2003
                                                                                  ACC70917;
                                                                                                                                                                                                                                                                                          Tanaka M;
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           20
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mEGES-1). The human meGES-1 gene is located on chromosome 9, more specifically to over the present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding meGES-1, which specifically hybridise with the nucleic acid encoding companies; (2) a method of inhibiting the expression of inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal continuation a disease or condition associated with meGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, cophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound combe used as used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or cophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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Alzheimer's disease, arthritis, diabetes, cancer, ischaemia, reperfusion injury, ophthalmic disorder, immunological disorder; cardiovascular disorder, neurological disorder; ss.
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Pred. No. 4.1e+04;
0; Mismatches 3;
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/note= "2'-0-methocyethyls"
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/note= "2'-0-methoxyethyls"
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                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antishabetic; immunomodulator, cardiant, neuroprotective, antishamatory, neuroprotective, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
                                                                                                                                                                       chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGBS-1; mPGBS-1 inhibitor; microsomal prostaglandin E2 synthase; imPGBS-1; mPGBS-1 inhibitor; introcessed and in E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nautiinflammatory; immunomodulatory; cardiavascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                                                                         Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "2'-0-methocyethyls"
16. .20
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                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mod_base= OTHER
                                   BP
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                                     ADM14505 standard; DNA; 20
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                                                                                                         01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                        ADM14505;
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RESULT 32
                      ADM14505/
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e.g.,

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF9-1] antisense oligonucleotide, (for Insulin-like Growth Factor [IGF9-3] corporation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF5151 and AAF45153-0190nucleotides of the present invention of the skin, a neoplasias, scleroderma, warfs, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; insulin-like Growth Factor. I receptor; IGF-1; pityriasis; IGF binding proctein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;
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can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                        Gaps
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                                                                                                                                               20;
                                                                                                                                               Length
                                                                                                                                                                                        Indels
                                                                                                                                               DB 12;
                                                                                                        Seguence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                               61.0%; Score 12.2; DB 12;
82.4%; Pred. No. 4.1e+04;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGFBP3 oligonucleotide #12.
                                                                                                                                                                                                                                   4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                                                                                                             19 rccrgcacgaagrggcr
                                                                                                                                                                                                                                                                                                                                                                                   AAF46592 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                            Conservative
                                                                                                                                                                Similarity
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Local S...
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Gaps

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Indels

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100.0%; Pred. No. 5.1e+04; Mismatches

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Best Local Similarity
                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBF3; inflammation; psoriasis; pitatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoolsis, neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neoblation of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                    Gaps
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                                                             Length 15;
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                      Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                         60.0%; Score 12; DB 4; Le
100.0%; Pred. No. 5.1e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edmondson SR;
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                                                                                                                                                                                                                                                                                  AAF46588 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       IGFBP3 oligonucleotide #8.
                                                                            Local Similarity 100.
nes 12; Conservative
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                                                                                                                                                                               12 gcaggaagcggc 1
                                                                                                                                          8 GCAGGAAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-041421/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wraight CJ,
                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001
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                                                                                                                                                                                                                                                                                                                         AAF46588;
                                                             Query Match
                                                                                                  Matches
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60.0%; Score 12; DB 4; Length 15;

Query Match

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The invention relates to a novel isolated 17 mer nucleic acid sequence, conclaining at least 15 consecutive mucleidides from the 17 mer sequence containing at least 15 consecutive nucleidides from the 17 mer sequence, a sequence with, after optimal alight at least 80 % identify to the 17 mer sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic caids of the invention are useful as probes and primers for detecting, dentifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for component of a gene chip, in vitro as (anti) sense reagents, and for component of a gene chip, in vitro as (anti) sense reagents, and for component of pharmaceuticals for prevention and/or treatment of vector or antibodies directed against the polypeptides are useful for vector or antibodies directed against the polypeptides are useful for prevention and/or treatment of viral diseases that are characterised by development of tumours or call case section, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in gene components of properties and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression the part of the nucleic acid sequences of the invention can be used in gene characy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic, virucide, neuroprotective, nootropic, neuroleptic, gene chip, antisense, sense, tumour, cell degeneration, cancer, Alzheimer's disease, schizophrenia, protein chip, gene therapy, tumour suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
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                                                                                                                                                                                                                                                                                                                                                                                                 ABT34760 standard; DNA; 17 BP.
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12; Conservative
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                                                                                                                                                                       15 CAGGAAGCGGCT
                                                                                      9 CAGGAAGCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABT34760;
                                                                                                                                                                                                                                                                                                           RESULT 35
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The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA crayments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing oligo. The isolated human can mix one further set of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also effect to a medical agent. The isolated human gene is also effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism cone of the invention.
                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide useful for detecting single nucleotide polymorphisms in human gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human biallelic marker downstream amplification primer SEQ ID NO:8500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 1567; 704pp; Japanese.
                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ74144 standard; DNA; 20 BP.
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                                                Homo sapiens.
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                                                                                                                                            26-AUG-2003
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                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                            ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           Human tumour suppressor seguence #3140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 765; 798pp; French.
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                                                                                                                                                                                            ACC54373 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TCTTGCAGGAAG 15
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                         2 ACTCTTGCAGGA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2004
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Matches
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                                                                                                                                                                                                                   SO CCC CCC CCC S S X L L L L X L X L X L X L X L X X L
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Gaps

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The present sequence is that of a labelled PCR primer used to amplify and genotype the partial nucleotide sequence of lipoprotein lipase precursor (LPL) surrounding the single-nucleotide polymorphism (SNP) - S site given in ABA02531. The specification describes a novel method for analysing a cvariant site (VS) in a target nucleotides a novel method for analysing a colymerase having 3'-5'-exonuclease activity. Ph is labelled on at least one nucleotide (nt) other than the 3'-terminal nt and it anneals to a region that spans VS in the first strand of NA. P2 is complementary to a cregion in the complementary second strand of NA. If P1 is complementary to to the base occupying VS it will be extended to form a labelled product. If P1 is not complementary the polymerase will digest P1 from its 3'-end, cremoving the label, and any setension product will be unlabelled. The extension products are analysed for absence/presence of the label. The method of the invention is particularly used to detect point mutations and SNRs, e.g. for diagnosis and prognosis of diabetes, thalassaemia, sickle-cell anaemia, cystic fibrosis or oncogenic mutations, or for and SNRs, e.g. for diagnosis and prognosis of diabetes, thalassaemia, sickle-cell anaemia, cystic fibrosis or oncogenic mutations, or for assessing predisposition to these conditions or monitoring the effect of treatments. Other applications are detecting pathogens (including those treatments and in prenatal testing or forensic investigations. The method can be used for simultaneous analysis of many different VS, in one or companie targets, providing very high throughput and rapid genotyping
                                                                                                            Analyzing variant sites in nucleic acid, useful e.g. for detecting disease-associated polymorphisms, comprises extension of labeled primer in presence of polymerase with 3'-5'-exonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribozyme; erythropoietin; granulocyte colony stimulating factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.0%; Score 11.8; DB 6; Length 16; 86.7%; Pred. No. 6.4e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hammerhead ribozyme substrate #3415.
                                                                                                                                                                                                                 Example 2; Fig 7C; 82pp; English
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                                                                    WPI; 2002-049286/06
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Best Local Similarity
                    Mathies RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200061729-A2.
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                    Xu H,
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                                                                                                                                                                                                                                                                                                                                   invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                             Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                    AAZ65654 to AAZ69578 represent human biallelic markers from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single-nucleotide polymorphism; SNP; diabetes; thalassaemia; sickle-cell anaemia; cystic fibrosis; oncogenic mutation; pathogen; paternity; prenatal testing; forensic investigation; genotyping; 3'-5'-exonuclease; point mutation; lipoprotein lipase precursor; LPL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%; Score 12; DB 3; Length 20; 75.0%; Pred. No. 5.2e+04;
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/mod base= OTHER
/note= "6-carboxy-x-rhodamine (ROX)"
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                                                                                                Chumakov I;
                                                                                                                                                                                                                                                                      Claim 8; Page 2043; 2745pp; English.
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98US-0109732P
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                                                                                                Blumenfeld M,
                                                                                                                                                                                                                      map of the human genome
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                                                                                                                                                WPI; 2000-013267/01
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; primer; ss.
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modified_base
                                                (GEST ) GENSE
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  23-NOV-1998;
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                                                                                                  Cohen D,
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Gaps

XX SQ Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other; Query Match 59.0%; Score 11.8; DB 3; Length 17; Best Local Similarity 86.7%; Pred. No. 6.4e+04; Matches 13; Conservative 0; Mismatches 2; Indels

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Gaps

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1 GACTCTTGCAGGAAG 15 |||| || || ||||| 1 GACTATTTCAGGAAG 15

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Sequence 19, App. Sequence 19, App. Sequence 1012, Ap Sequence 1350, Ap ?equence 1351, Ap ?equence 1351, Ap ?equence 1348, Ap
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Sequence 79, Appl
Sequence 8114, Ap
Sequence 844, App
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11 US-10-773-678-339

12 US-10-773-678-339

13 US-10-773-678-19

14 US-10-773-678-19

15 US-10-773-678-19

16 US-10-339-674-1350

17 US-10-339-674-1349

18 US-10-318-316-79

18 US-10-318-316-79

18 US-10-671-395-571

28 US-10-671-395-571

29 US-10-671-395-571

20 US-10-714-796-161

20 US-10-714-71-71

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cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

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cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*

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cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

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US-10-773-678-179
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US-10-857-715-201
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US-10-773-678-341
; Sequence 341, Application US/10773678
; Publication No. US20080074879A1
; General Description No. US20080074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Expression
; FILE REPERENCE: ISPH-0828
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/10/713,678
; PRIOR PILING DATE: 2001-01-11
; PRIOR PILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-04-06
; PRIOR FILING DATE: 2000-04-06
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; NUMBER OF SEQ ID NOS: 402
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Publication No. US20050074879A1
GENERAL INFORMATION:
APPLICANT: Karras, James G
TILLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
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Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense oligonucleotide US-10-773-678-179
PRIOR APPLICATION UNMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR PELING DATE: 2003-11-14
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR PELING DATE: 1999-04-08
NUMBER: OF SEQ ID NOS: 402
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 179
LENGTH: 20
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100.0%; Pre
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 19; Conservative
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LENGTH: 20
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6215, Ap
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Sequence 342, Application US/10773678

Publication No. US2005007487941

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
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APPLICANTION:
APPLICANTION:
APPLICANTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANTION:
FILE REFERENCE: ISPH-0828

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT APPLICATION NUMBER: US/10/713,139

PRIOR APPLICANTION NUMBER: 09/713,139

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2001-01-14

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SOFTWARE: PATENTIN VENT OF 12

SEQ ID NO 342

LENGTH: 20
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US-10-773-678-179
Sequence 179, Application US/10773678
Publication No. US20050074879A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antiense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
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US-10-723-361-116

US-10-723-361-118

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US-10-723-361-6215

US-10-723-361-6215

US-10-723-361-6216

US-10-723-361-6219

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US-10-723-361-6219

US-10-723-361-6219

US-10-723-361-6219

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US-10-733-762-6247

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ORGANISM: Artificial Sequence
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Best Local S:
Matches 20
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Gaps

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JOURNALL ANNOVATION: James G
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/713,678
PRIOR APPLICATION NUMBER: US/10/713,139
PRIOR APPLICATION NUMBER: 09/758,881
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 402
SOFTWARE: PATENTIN VOIL 1999-04-08
NUMBER OF SEQ ID NOS: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 201, Application US/10857715
; Sequence 201, Application US/10857715
; Publication No. US20050164218A1
; GENERAL INFORMATION:
; APPLICAMT: Aqus David
; APPLICAMT: Baker Joffre
; APPLICAMT: Baker Joffre
; APPLICAMT: Bake Steven
; TITLE OF INVENTION: Gene Expression Markers for Response to
; TITLE OF INVENTION: Gene Expression Markers for Response
; TITLE OF INVENTION: Gene Expression Markers
; FILE REFERENCE: 39740/0011
; CURRENT FILING DATE: 2004-05-28
; PRIOR FILING DATE: 2004-05-30
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201
: LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 20; 73;
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80.0%; Score 16; DB 22; L
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0;
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, OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-344
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85.0%; Score 17; DB
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches
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; Publication No. US20050074879A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: reverse primer US-10-857-715-201
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-773-678-339
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Sequence 340, Application US/10773678

Publication No. US20050074879A1

GENERAL INFORMATION:
APPLICANT: Karras, James G

TITLE OF INVENTION: Expression
FILE REFERENCE: ISH-0828

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT APPLICATION NUMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SEQ ID NO 340

LENGTH: 20
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CTHER INFORMATION: Antisense oligonucleotide

US-10-773-678-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343
            FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 402
SOFTWARE: Patentin Ver. 2.1
SENGTH: 20
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Expression
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
TITLE OF INVENTION:
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# TITLE OF INVENTION: Antisense Oligonuclectide Modulation of STAT3

# TITLE OF INVENTION: Expression

# CURRENT FILING DATE: 2004-02-06

# PRIOR PILING DATE: 2003-11-14

# PRIOR APPLICATION NUMBER: PCT/US00/09054

# PRIOR FILING DATE: 2001-01-11

# PRIOR PILING DATE: 2000-04-06

# PRIOR FILING DATE: 1999-04-08

# NUMBER OF SEQ ID NOS: 402

# SEQ ID NO 345

* LENGTH: 20
APPLICANT: Karras, James G

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

TITLE OF INVENTION: Expression

FILE REPERENCE: ISPH-0028

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT PILING DATE: 2004-02-06

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2001-01-11-19

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SOOFWARE: Patentin Ver. 2.1

SEQ ID NO 339
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US-10-773-678-339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 345, Application US/1073678
Publication No. US20050074879A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 15; Conservative
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Matches 15, Conservative
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Sequence 19, Application US/09758881

Sequence 19, Application US/09758881

Patent No. US2001029250A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Antisense Oligonuclectide Modulation of STAT3

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-0532

CURRENT APPLICATION NUMBER: US/09/758,881

CURRENT PILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR APPLICATION NUMBER: 1099-04-06

PRIOR FILING DATE: 1099-04-08

NUMBER: OF SEQ ID NOS: 152

SEQ ID NO 19

LENGTH: 20

LENGTH: 20
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TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT PILING DATE: 2004-02-06
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-773-678-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/10773678; Publication No. US20050074879A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 20
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US-10-773-678-19
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RESULT 12 US-10-671-395-1012/c

RESULT 10

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; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber
US-10-339-674-1348
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Publication No. US20030204318A1

GENERAL INFORMATION:
APPLICANT Feldmann, Richard J.; Global Determinants, Inc.
TITLE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674

CURRENT PILING DATE: 2003-06-06

NUMBER OF SEQ ID NOS: 3537

SEG ID NO 1349

LENGTH: 19
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Publication No. US20030204318A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION:
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SOFTWARE: Proprietary
SEQ ID NO 1348
LENGTH: 19
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64.0%; Score 12.8; DB 17; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                 Length 18;
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Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels
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ORGANISM: Escherichia coli K-12 MG1655 complete genome
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                                             TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome
                                                                                                                                                                                                            Ouery Match 64.0%; Score 12.8; DB 17;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2;
                                                                                             ; FEATURE:
; LOCATION: (1734068)...(1734085)
; OTHER INFORMATION: Chromosome = 1
US-10-339-674-1351
                                                                                                                                                                                                                                                                                                                 4 TCTTGCAGGAAGCGGC 19
                                                                                                                                                                                                                                                                                                                                             2 TCTTGCCGGATGCGGC 17
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US-10-339-674-1349
SEQ ID NO 1351
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                    Publication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Glerse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . LOCATION: (1734068)...(1734084)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = US-10-339-674-1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1350, Application US/10339674
Sequence 1350, Application US/10339674
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SOFTWARE: Proprietary
SEQ ID NO 1350
LENGTH: 17
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TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SOFTWARE: Proprietary
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Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.0%; Score 13.6; DB 19;
80.0%; Pred. No. 4.4e+03;
ive 0; Mismatches 4;
                                                                                                                                                            FILE REPRENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Human PGE2 antisense
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  Sequence 1012, Application US/10671395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CACTCTTGCAGGAAGCGGCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: artificial
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US-10-339-674-1350/c
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US-10-339-674-1351
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Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity, and Methods
of Use Thereof
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                                                                                                                                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFWARE: FastERD for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
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ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto
CITY: Palo Alto
COUNTY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR PAPELICATION:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/081,385
FILING DATE: 05/081,385
FILING DATE: 06/080,1997
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 06/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WM. Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20
TELEPHONE: 650-813-5600
TELEPHONE: 650-813-5600
      TITLE OF INVENTION: Factors Alterin
TITLE OF INVENTION: Factor Receptor
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 14; Conserva
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US-10-967-092-134
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APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: Of Use Thereof
TITLE OF INVENTION: Of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTY: USA
COUNTY: USA
ADDRESSEE: MORRISON WILL ROAD
CITY: Dalo Alto
STATE: CA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING PATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
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64.0%; Score 12.8; DB 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 134, Application US/09984198
Patent No. US20020106679A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
                                                                                                                                                           Sequence 134, Application US/09752639
Patent No. US20020091243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELERAX: 650-494-0792
TELERAX: 706141
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
             TCTTGCAGGAAGCGGC 19
                                                   2 rcrreccedarecede 17
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Sequence 571, Application US/10671395
; Sequence 571, Application Wo. US20040132063A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT APPLICATION NUMBER: 60/413,549
; PRIOR APPLICATION NUMBER: 60/413,549
; RIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 571
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Pred. No. 1.5e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.0%; Score 12.8; DB 24; Best Local Similarity 87.5%; Pred. No. 1.1e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
             FILING DATE: 13-Nov-2000
APPLICATION NUMBER: US/09/081,385
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WU, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-11-011-500-134
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                                                                                                                                                                                                                                                                                 TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                              TELEX: 706141
INFORMATION FOR SEQ ID NO: 134:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TCTTGCAGGAAGCGGC 19
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-671-395-1013/c
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Publication No. US20050158826A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/011,500

FILING DATE: 13-Dec-2004

CLASSIFICATION DATA:
                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.0%; Score 12.8; DB 21; Best Local Similarity 87.5%; Pred. No. 1.1e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/712,813
FILING DATE: 13-NOV-2000
APPLICATION NUMBER: US/09/081,385
FILING DATE: cUhknown>
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WU, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/967,092
FILING DATE: 15-Oct-2004
                                                                                 CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/967,092
FILING DATE: 15-Oct-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-10-967-092-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 134:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING KCNEI AS AN LQT GENE
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Connors, Timothy D.
APPLICANT: Splawski, 1907
TITLE OF INVENTION: KVLQTI - A LONG QT SYNDROME GENE TITLE OP INVENTION: KVLQTI - A LONG QT SYNDROME GENE TITLE REFERENCE: 2323-163
CURRENT APPLICATION NUMBER: US /10/368,643
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/597,731
PRIOR APPLICATION NUMBER: US 09/135,010
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-08-17
PRIOR PLING DATE: 1998-07-29
PRIOR FILING DATE: 1999-08-29
PRIOR FILING DATE: 1999-08-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-11-222
MIMMER OF SED IN NOWBER: US 60/019,014
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Pred. No. 1.9e+04;
0; Mismatches 1;
TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPT TITLE OF INVENTION: KCNE1 AS AN LQT GENE CURRENT APPLICATION NUMBER: US/10/138,316 CURRENT FILING DATE: 2002-05-06 PRIOR PRIOR PILING DATE: 1999-11-22 PRIOR PILING DATE: 1999-08-17 PRIOR FILING DATE: 1999-08-17 PRIOR FILING DATE: 1999-08-17 PRIOR PILING DATE: 1999-08-17 PRIOR PILING DATE: 1999-08-17 PRIOR PILING DATE: 1997-08-29 PRIOR PILING DATE: 1997-08-29 PRIOR PILING DATE: 1996-08-17 PRIOR PILING DATE: 1996-10-29 PRIOR PILING DATE: 1996-10-29 PRIOR PILING DATE: 1996-10-29 PRIOR PILING DATE: 1996-12-22 PRIOR PILING DATE: 1996-10-29 PRIOR PILING DATE: 19
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Publication No. US20030170708A1
GENERAL INFORMATION:
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92.9%;
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92.9%;
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 92.9
Matches 13; Conservative
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Matches 13; Conservative
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US-10-368-643-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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          APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Publication No. US20030054380A1
CENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, Igor
IITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN minK WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1512, Application US/10984919
Fublication No. US20050130927A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Brysch, Wolfgaug
TITLE OF INVENTION: ANTISENSE CLIGONUCLEOTIDE PREPARATION METHOD
FILE REFERENCE: 10496/P63763180
CURRENT FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US/10/9341,700
PRIOR PILING DATE: 1999-02-24
PRIOR PLILING DATE: 1999-02-24
PRIOR PLILING DATE: 1999-01-30
PRIOR PILING DATE: 1999-01-30
PRIOR PILING DATE: 1999-01-31
NUMBER OF SEQ ID NOS: 1764
SOFTWARE: Patentin Ver. 2:1
LENGTH: 17
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, OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1512
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Pred. No. 1.9e+04;
0; Mismatches 1;
                                                                                                  FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PatentIn version 3.2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Human PGE2 antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ACTCTTGCAGGAAGCGGCT 20
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Best Local Similarity 92.9%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: artificial
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APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE
TITLE OF INVENTION: MUMBER: US/10/911,678
TITLE OF INVENTION: CAUSE ARRHYTHMA SUSCEPTIBILITY THEREBY ESTABLISHING
FILE REPERENCE: 2323-16
PRIOR FILING DATE: 1999-11-2-2
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1995-10-2-2
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE AS AN LOT GENE
FILE REFERENCE: 2323-167
CURRENT APPLICATION NUMBER: US/10/861,520
CURRENT PILING DATE: 2002-05-06
FRIOR APPLICATION NUMBER: 09/444,295
FRIOR APPLICATION NUMBER: 09/135,020
FRIOR APPLICATION NUMBER: 08/921,068
FRIOR APPLICATION NUMBER: 08/921,068
FRIOR FILING DATE: 1998-08-17
FRIOR PILING DATE: 1996-10-29
FRIOR FILING DATE: 1995-12-22
FRIOR FILING DATE: 1995-12-22
FRIOR FILING DATE: 1995-12-22
FRIOR FILING DATE: 1995-12-22
FRIOR FILING DATE: 1998-07-29
FRIOR FILING DATE: 1998-07-29
FRIOR FILING DATE: 1998-07-29
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Pred. No. 1.9e+04;
0; Mismatches 1;
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; Publication No. US20050003439A1
; GENERAL INFORMATION:
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92.9%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 recadeadaddar 5
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Best Local Similarity 92.9
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-10-911-678-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-10-861-520-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-911-678-79/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                   Sequence 129, Application US/10714796

| Sequence 129, Application US/10714796
| Publication No. US20040180847A1
| Publication No. US20040180847A1
| GENERAL INFORMATION:
| APPLICANT: Dobie, Kenneth W. | APPLICANT: Koller, Exich | APPLICANT: Koller, Exich | APPLICANT: MATISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION | TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION | FILE REFERENCE: ISHT-1004 | CURRENT PILING DATE: 2003-11-17 | CURRENT PILING DATE: 2003-11-17 | PRIOR FILING DATE: 2002-05-23 | NUMBER OF SEQ ID NOS: 237 | SOFTWARE: Patentin version 3.2 | SEQ ID NO 129 | LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16.1 Application US/10714796
; Sequence 16.1 Application US/10714796
; Publication No. US20040180847A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: KOller, Erich
; TITLE OF INVENTION: ANTIENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
; FILE REFERENCE: ISHT-1004
; CURRENT PAPLICATION NUMBER: US/10/714,796
; CURRENT PILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
: LENGTH: 20
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Pred. No. 1.9e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 19;
Pred. No. 1.9e+04;
0; Mismatches 1;
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Sequence 79, Application US/10861520
Publication No. US20040235038A1
GENERAL INFORMATION;
APPLICANT: Reating, Mark T.
APPLICANT: Sanguinetti, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.0%;
92.9%;
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Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TCTTGCAGGAAGCG 17
                  TGCAGGAAGCGGCT 20
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Mus musculus
US-10-714-796-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA; ORGANISM: Homo sapiens
US-10-714-796-129
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APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANDON, MAIK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
TITLE OF INVENTION: HUMAN WOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REPERENEE: PB0105
CURRENT PILING DATE: 2003-11-26
PRIOR PILING DATE: 2003-11-26
PRIOR FILING DATE: 2000-10-5-25
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/206, 359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PADM.
PROPARATION NUMBER: PCT/USO1/00669
PRIOR PRIOR PRIOR PRIOR PRIOR PADM.
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR PADM.
PROPARATION NUMBER: PCT/USO1/00669
PRIOR PRIOR PADM.
PROPARATION DATE: 2001-01-30
PRIOR PRIOR PADM.
PROPARATION DATE: 2001-01-30
PRIOR PRIOR PADM.
PROPARATION DATE: 2001-01-30
PRIOR PADM.
PROPARATION DATE:
                              Sequence 544, Application US/09730289B
; Sequence 544, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: McHodd and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MSHB00-864-A (400/006)
; CURRENT FILING DATE: 2000-12-05
; RIOR APPLICATION NUMBER: US 60/169,100
; RIOR FILING DATE: 1999-12-06
; NUMBER: OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 544
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Publication No. US20040137589A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PLI, Yonggang
APPLICANT: PENN, Sharron G,
APPLICANT: HANZEL, David K.
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Best Local Similarity 82.4<sup>‡</sup>
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Homo sapiens
US-09-730-289B-544
                          IS-09-730-289B-544/C
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APPLICANT: CHEN, WENDERING

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILLE REPERENCE: AECONICA-7

CURREMY PILING DATE: AECONICA-7

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-27

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PPLICATION NUMBER: US 60/266, 860

PRIOR PPLICATION NUMBER: US 60/266, 860
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                   Score 12.4; DB 21; Length 20; Pred. No. 1.9e+04; 0; Mismatches 1; Indels C
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SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 8114
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8114, Application US/09866108
Patent No. US20020048800A1
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92.9%;
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APPLICANT: JI, Yongaang
PPLICANT: PENN, Sharzon G.
APPLICANT: HANZEL, David K.
Query Match
Best Local Similarity 92.5.
Local 31 Conservative
                                                                                                                                                                                                                                                             18 TGCAGGAAGCGGAT 5
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CORGANISM: Homo sapiens
US-09-866-108-8114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               -09-866-108-8114
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APPLICANT:
APPLICANT:
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APPLICANT: Cohen, Daniel
APPLICANT: Chuenfeld, Marta
APPLICANT: Blumenfeld, Marta
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REPERENCE: GENSET.020CP1
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US-10-719-956-271624/c
US-10-719-956-271624, Application US/10719956

; Sequence 271624, Application US/10719956
; Publication No. US20040146910A1
; GRERRAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TITLE APPLICATION UNMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR PAPLICATION NUMBER: 60/427,836
; RIOR APPLICATION NUMBER: 60/427,836
; RIOR APPLICATION PROPE: 5002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SEQ ID NO 271624
; LENGTH: 20
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                                                                                                                                                                                                                  APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT APPLICATION NUMBER: 60/427,808
PRIOR PILING DATE: 2002-11_20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 383106
LENGTH: 20
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Best Local Similarity 82.4%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 3;
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Pred. No. 2.4e+04;
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                                                                                                                                                         ; Sequence 383106, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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Sequence 8500, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:
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4 TCTTGCAGGAAGCGGCT 20
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11 Similarity 82.4%;
14; Conservative (
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                                            19 rccrecaceaagreecr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus
US-10-719-900-383106
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Best Local Similarity
                                                                                                                    RESULT 35
US-10-719-900-383106/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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; Sequence 692, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE WOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE US/10/671,395
TITLE OF INVENTION: ANTISENSE US/10/671,395
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                Sequence 507, Application US/10671395
; Sequence 507, Application US/10671395
; Bublication No. US20040132063A1
; GENERAL INFORMATION:
    APPLICANT: Paramacia Corp.
; APPLICANT: Glerse, James K
    TITLE OF INVENTION: EXPRESSION
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 11791/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR PILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO SO77
: LENGTH: 20
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                                                                  Score 12.2; DB 19;
Pred. No. 2.4e+04;
0; Mismatches 3;
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Best Local Similarity 82.4%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                    0; Mismatches
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-692
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-507
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                                                                     Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
; ORGANISM: Homo sapiens US-10-723-361-8114
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Sequence 997, Application US/09780533A
; Sequence 997, Application No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TILE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; TILE REFERENCE: MBHB00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780, 533A
; CURRENT FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; MUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 997
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    TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
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86.7%; Pred. No. 3.8e+04;
iive 0; Mismatches 2;
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                         FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
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Best Local Similarity 86.7
Warches 13; Conservative
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US-09-780-533A-997
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 13; Conserv
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; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-15968 for SEQ 635, in compleme
US-10-349-143-8500
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Sequence 91, Application US/09780533A

Publication No. US2030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Chowrira, Bharat
APPLICANT: Habberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: BHBHB00, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT APPLICATION NUMBER: US 60/181,797

PRIOR FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR PELING DATE: 1999-10-20

PRIOR PELING DATE: 1999-10-20

PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

LENGTH: 20
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Best Local Similarity 75.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 5; Indels
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Pred. No. 3.8e+04;
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; Sequence 92, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Haeberli, Pete
; APPLICANT: Haeberli, Pete
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SOFWARE: Patentin version 3.0
SEQ ID NO 91
LENGTH: 17
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Best Local Similarity 86.7
Matches 13; Conservative
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ORGANISM: Homo sapiens
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66
86
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Contact: Robert B. W
University of Utah C
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 0031 row: G column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ314365
AZ314365.1 GI:10360181
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0031 row: G column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IM0031G07F Mouse 10kb plasmid
clone UUGC1M0031G07 F, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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37.0
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Location/Qualifiers
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                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative of pMP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and the character of moving number of the character o
                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
                        purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F /Clome_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: FWPA2ny; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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Query Match

53.0%;

Score 10.6;

DB

8

Length 20;

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REFERENCE
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AJ650912
                               Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embryo development in pigs and
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, S.I., Finlayson, H.A. and Archibald, A.L. Development of cDNA and EST resources for studying embryo development in pigs and cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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EST.
                                                                                                                                      Arabidopsis thaliana (thale cress)
                                                                                                                                                                                    CD532073.1 GI:40452085
                                                                                                                                                                                                                                                       13I04 Arabidopsis Leaf Senescence Library Arabidopsis thaliana
                                                                                                                                                                                                                                                                                 CD532073
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Roslin, Midlothian,
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(bases 1 to 19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003276_L01"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSEQRAN19 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBlueScript11(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"
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91.7%;
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  and Gan, S
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); Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10.4; DB 1; Length 18; Pred. No. 2e+06;
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cofa cDNA clone C0003276_L01,
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Tel: 607 254 5418
Fax: 607 255 0599
                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0497 row: D column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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AZ637794.1 GI:11759984
GSS.
Mus musculus (house mouse)
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1M0497D20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0497D20 F, genomic survey sequence
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                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 20)
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Insert Length: 19
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                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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quality sequence stop: 20
Location/Qualifiers
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                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
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/dev_stage="Yellow Leaf With Greenish Base Area"
/lab_host="E. coli"
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/mol_type="mRNA"
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1.6e+06;
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0

Plate: 0066 row: J column: 13

Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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20 bp DNA linear GSS 29-SEP-200
1M0066J13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0066J13 R, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Pred. No. 2.6e+06;
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                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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19 bp DNA linear GSS 0:
1M0182L02R Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0182L02 R, genomic survey sequence.
                                                                       Seq primer: CACACAGGAAACAGCTATGACC
                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: L column: 02
                                                                                                                                                                     Tel: 801 585 5606 Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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                                             Class: plasmid ends
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quality sequence stop: 19.
Location/Qualifiers
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adaptored vector DNA, and transfer and into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0085 row: E column: 05
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Seq primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
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University of Utah
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                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0055 row: H column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Mus musculus (house mouse)
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University of Utah
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Contact: Robert B.
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Fax: 801 585 7177
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/clome_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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   Email: ddunn@genetics.utah.edu
Insert i.ength: 10000 Std Error: 0.1
Plate: 0307 row: L column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ACTCTTGCATG
                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1M0307L16R Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0307L16 R, genomic survey sequence.
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Unpublished (2000)
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                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                     84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ482658.1 GI:10645919
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                     USA
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0055H05"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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                                                                                                                                                                                Std Error: 0.00
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smid UUGC1M library Mus musculus genomic
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GSS 05-OCT-2000

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                                                                                                                                                                                                                                                                                                                                                 Pristionchus pacificus
Nucleic Acids Res. 32 (1),
Contact: Sommer RJ
                                                                                                                                                            Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                             Max-Planck-Institute for Developmental Spemannstr. 37-39, Tuebingen D-72076, GTel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                                          Srinivasan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pristionchus pacificus
Pristionchus pacificus
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                                                                                                                                                                                                                                                                                                                                Evolutionary Biology
                                                                                                                                                                                                                                                                                                                                                                                                                  Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CL661094.1 GI:50147102
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                                                                                                                                         primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwp42 (gi|47321/4|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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/strain="C57BL/6J"
                                                                                           location/Qualifiers
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Pred. No.
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Germany
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BX559186
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Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
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ω
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                                                                                                                                                                                                                                                                                                                                                                                                               School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with swifts ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glossina morsitans morsitans
Glossina morsitans morsitans
Glossina morsitans morsitans
Elastyota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.

1 (bases 1 to 20)

Ciboon of Verbornon A Regrimman M.
                                                                                                                                                                                                                                                                                                                                                                          All clones with suffix qlc are reverse end of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX559186 Glossina morsitans morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response genes
Genome Biol. 4 (10), R63 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14519198
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                                                                                       Similarity
                                   CTCTTGCAGGAAGCGGC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTGCAGGAAGCGGCT 20
CTCTAGTAAGAAGTGAC 19
                                                                     Conservative
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var. California"
                                                                                                                                                                                                             /clone="Tse42b02 q1c"
/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected
                                                                                                                                                              /note="country: Zimbabwe;
r.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pEpifos-5 Fosmid vector"
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                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/sub_species="morsitans"
                                                                                                                                                                                                                                                                                                                         organism="Glossina morsitans"
                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                         xref="taxon:37546"
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Pred. No. 1e+0
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1e+07;
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BQ587767.1
                                   1M0302N15R Mouse 10kb plasmid TUGCIM library Mu
clone UUGCIM0302N15 R, genomic survey sequence.
AZ481008
AZ481008.1 GI:10641989
GSS.
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1 (bases 1 to 16)
1 (bases 1 to 16)
1 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski, M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ587767 16 bp mRNA linear EST 06-DEC E012340w-024-010-M01-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-010-M01 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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Plate: 10 row: M column: 01
Seq primer: SP6; CATACGATTTAGGTGACACTATAG
Mug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: weisshaa@mpiz-koeln.mpg.de
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musculus
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                   musculus (house mouse)
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/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saarzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                               RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-Notl-T7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GABI:185096"
/db_xref="taxon:161934"
/clone="024-010-M01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
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/cultivar="KWS2320 (double haploid, monogerm breeding
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83.3%;
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Pred. No. 1.2e+07;
0; Mismatches 2;
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mid UUGC1M library Mus
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                                                                                         AZ959942 19 bp DNA linear GSS 47-AFK-200
2M0227L13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0227L13 R, genomic survey sequence.
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High quality sequence stop: 19.
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Insert Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/clone="UUGC1M0302N15"
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/strain="C57BL/6J"
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                                                  GI:13831169
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83.3%;
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Pred. No. 1.2e+07;
0; Mismatches 2
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Tel: 8
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University of Utah Genome Center
University of Utah
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AJ599745
AJ599745.1 GI:37949373
GSS; left border; T-DNA flanking sequence
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CACACAGGAAACAGCTATGACC
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Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: L column: 13
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                 AJ599745 20 bp DNA li
Arabidopsis thaliana T-DNA flanking sequence,
492G09, genomic survey sequence.
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Location/Qualifiers
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Fax: 801 585 7177
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                                                                                                                                                                                                                                          TATTCCACCAAG 2
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                                                                                                                                                                                                                                                                                                                                                                                                            adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_bost="E. coli strain XL10-Gold, T1-resistant,
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/).
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/clone="UUGC2M0227L13"
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/strain="C57BL/6J"
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83.3%;
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Best Local Similarity
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AJ587896
AJ587896.1 GI:37937520
AJ587896.1 GI:37937520
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
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PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 bp 1
Arabidopsis thaliana T-DNA flanking
337H10, genomic survey sequence.
AJ587896
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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Direct Submission
                                                                                              Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Lepiniec, L., Caboche, M. and Lecharny, A.
                                                                 I-DNA integration into the Arabidopsis
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pre-insertion sites
BO Rep. 3 (12), 1152-1157 (2002)
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left border"
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/clone="492G09"
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'cultivar="Wassillewskija"
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Pred. No. 1.6e+07;
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Rose,R., Pelletier,G.,
                                                                    genome depends on sequences
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Best Local Similarity
Thes 9; Conserve
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AZ397615/c
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AZ397615.1 GI:10512687
GSS.
Mus musculus (house mouse
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0162 row: M column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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19 bp DNA linear GSS 03-OCT-200
1M0162M07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0162M07 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
Unpublished (2000)
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                                                                High quality sequence stop: 19
                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                       University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                       lass: plasmid ends
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/organism="Mus musculus"
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left border"
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/mal_type="genomic DNA"
/cultiva="Wassillewskija"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                     Weiss
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Pred. No. 1.9e+07;
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AUTHORS
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SOURCE
ORGANISM
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AZ413661/c
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DEFINITION
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Best Local
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                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 TTACAGGAAG
                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0197 row: I column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
                                                           Location/Qualifiers
/organism="Mus musculus"
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Pred. No. 2e+07;
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                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: I column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
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                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                                                                          quality sequence stop: 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
organism="Mus musculus"
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/clone="UUGC1M0197I07"
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RESULT 19

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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                            Imail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0410 row: N column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0410N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0410N24 R, genomic survey sequence
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9; Conserve
                                                                       High quality sequence stop: 20
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                              University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B.
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                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA'
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552123"
/organism="Mus musculus"
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Pred. No. 2e+07;
0; Mismatches
                                                                                                                                                                           Std Error: 0.00
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RESULT 21
AZ827842
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                         source
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone UUGC2M0104F03 R, genomic survey sequence. AZ827842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ827842.1 GI:12997750
GSS.
                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: F column: 03
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                        University of Utah C
University of Utah
Rm. 308, Biomedical
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                                                                                                         Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
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                                                   quality sequence stop: 20.
Location/Qualifiers
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801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
10.5 kb range using preparative agarose gel
10.5 kb range using preparative agarose
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone="UUGC1M0410N24"
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/strain="C57BL/6J"
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/organism="Mus musculus"
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90.0%;
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KEYWORDS

FEATURES

COMMENT

COMMENT

TITLE

FEATURES

Vector R.Site 1 R.Site 2

: pBACe3.6 : EcoRI

te 2 : EcoRI. Location/Qualifiers

TITLE

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ORIGIN

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TITLE
JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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AG189193/c
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3 (bases 1 to 20)
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AG189193
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG189193 20 bp DNA linear GSS 06
Pan troglodytes DNA, clone: RP43-063J03.T7, genomic survey
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                                                                                                                           of clone tracking errors.
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                               Sequencing: T7
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGCIM library
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Project (CGAP),

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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
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1 (Dases 1 to 13)

1 (Bases 1 to 13)

2 (Bases 1 to 13)

2 (Bases 1 to 13)

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8 (Bases 1 to 13)

9 (Bases 1 to 13)

1 (Bases 1 to 13)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ789829
BQ789829.1 GI:22004791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hage002aH08 Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion annosum mixed EST library cDNA clone hage002aH08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ789829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Fred.Asiegbu@mykopat.slu.se
                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                               6 days with H. annosum" - Scots pine infection /clone lib="Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library" | Stage (HAGE) subtraction cDNA library" The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="hage002aH08"
/dev_stage="Seedling roots of scots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Pinus sylvestris/Heterobasidion annosum mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
'db_xref="taxon:169015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T7 primer
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Pred. No. :
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Pred. No. 2.3e+07;
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KEYWORDS
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AUTHORS
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ORGANISM
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                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                            sequence.
C00629
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI042533 18 bp mRNA linear 0y06e03.x1 Soares senescent fibroblasts NbHSF Homo clone IMAGE:1665052 3' similar to TR:015662 Q15662 TRANSFORMATION-RELATED PROTEIN ;, mRNA sequence.
                                                                           BodyMap; human gene
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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EST.
                             Contact: Okubo, K.
Institute for Molecular
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 18)
                                                                                                                                                                                                                                                                                                                                                                                               HUMGS0008172 Human adult (K.Okubo)
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     Osaka University
                                                                                                                              Okubo, K.
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="senescent fibroblast"
/lab_host="PH108 (ampicillin resistant)"
/clone_libe="Soares_senescent_fibroblasts_NbHSF"
/clone_tibe="Soares_senescent_fibroblasts_NbHSF"
/note="Vector: p7773D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; lst_strand_cDNA was primed_with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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76.9%;
                                                                                                      expression database
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Pred. No. 2.4e+07;
                             and Cellular Biol
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Homo sapiens cDNA, mRNA
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Gaps

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EST 31-DEC-2002

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JOURNAL COMMENT
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CL661466
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VERSION
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                          Indi: ralf.sommer@ruebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CL661466
CL661466.1 GI:50147979
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-3, Yamada-oka, Suita,
Tel: 06-877-5111(ex.331
Email: kousaku@imcb.osa
                                                                                                                                                                                                                                                                                                                                                                                             Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppaDB: an AcedB database for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus
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Pristionchus pacificus
1 GACTCTTGCAGGA 13
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                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             survey sequence.
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                                                                                                                                                /db_xref="taxon:54126"
/clone_lib="Mixed stage
var. California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
                                                                                                                                                                                                       /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="One or more human adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                /note="Vector: pEpifos-5
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76.9%;
                                                     41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           līb="Human adult (K.Okubo)"
"One or more human adult tissue"
                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8.2; DB 6;
Pred. No. 2.4e+07;
0; Mismatches 3
                                   Score 8.2; DB 9;
Pred. No. 2.4e+07;
0; Mismatches 3
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stage fosmid library of P.
pacificus genomic, genomic
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$014305-024-010-H05-SP6 MPIZ-ADIS-024-leaf

024-010-H05 5-PRIME, mRNA sequence.

BQ587387

BQ587387.1 GI:26116969
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Roslin, Midlothian, EH25 9PS, Www.arkgenomics.org.
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 19)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying
embryo development in pigs and cattle
Unpublished (2004)
                                                                            Beta vulgaris
Beta vulgaris
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Genomics and Bioinformatics
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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Sus scrofa
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Construction of a 'unigene' cDNA clone fingerprinting allows access to 25 000
                                  and Radelof, U.
                                                Drungowski,M., Stahl,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
/mol type="mana"
/mol type="mana"
/db xref="taxon:9823"
/clone="C0000033_N10"
/tissue_type="placenta"
/clone_Tip="CSEQRAN09"
/clone_Tip="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
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D., Wruck,W., Menze,A., O'Brien,J., Leh
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Pred. No. 2.4e+07;
0; Mismatches 3
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                                                                          Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical I
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22362189
12472698
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                       1M0109P06R Mouse 10kb plasmid clone UUGC1M0109P06 R, genomic AZ363824 GI:10477524 GSS.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacze, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: weisshaa@mpiz-koeln.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Weisshaar
                                                                                                                                                         plasmid inserts
Unpublished (200
                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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te: 10 row: H column: 05
primer: SP6; CATACGATTTAGGTGACACTATAG
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                                                                                                                                                                                               whole genome scaffolding with paired end reads from 10kb
ddunn@genetics.utah.edu
                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="MPIZ-ADIS-024-leaf"
/note="Vector: pcMvSPORT6; Site 1: Sall; Site 2: Notl;
/note="vector: pcMvSPORT6; Site 1: Sall; Site 2: Notl;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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/lab_host="EMDH10B"
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/mol_type="mRNA"
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/db_xref="taxon:161934"
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                                                                                                                     Genome Center
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                                                                              Polymers Research
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                University of Utah University of Utah
                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                  Unpublished (2000)
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                                                                                             308,
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                                                                    USA
ddunn@genetics.utah.edu
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                                                                                          Biomedical Polymers Research Bldg.,
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/clome_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from I
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/strain="C57BL/6J"
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                                                                                                                                         Genome Center
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Pred. No. 2.4e+07;
0; Mismatches 3;
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  84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Nouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1)
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seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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19 bp DNA linear GSS 05-OCT-2011M0351A21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0351A21 R, genomic survey sequence.
                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                       plasmid inserts
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AZ509071.1 GI:10690387
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                                                                                                                                                                                                Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ddunn@genetics.utah.edu
                                                                                                  Biomedical
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0201P12"
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/strain="C57BL/6J"
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Pred. No. 2.4e+07;
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Plate: 0351 row: A column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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AZ626779
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                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                      Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                        Tel: 801 585 5606
Fax: 801 585 7177
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Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/) as hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone="UUGC1M0351A21"
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/strain="C57BL/6J"
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                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                      Unpublished (2000)
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ddunn@genetics.utah.edu
                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0467A14"
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76.9%;
                                                                                             Polymers Research
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T. brucei sheared genomic genomic survey sequence.
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution ( 4 kb). The v + i method used for the library construction is described in detail in Smatth, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In
                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACTCTTGCAGGA 13
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                                                                                                                                                                                         nh1@sanger.ac.uk
                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWp42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No. 2.5e+07;
0; Mismatches 3;
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AA916934/c
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ORGANISM
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Details of T. brucei sequencing at the Sanger Centre
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACTCTTGCAGGA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality Insert Length: 444 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)
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EST.
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similar to SW:BI3_MOUSE
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH108"
/clone lib="NCI CGAP_LU5"
/clone lib="NCI CGAP_LU5"
/clone lib="NCI CGAP_LU5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a /note="Organ: lung; Vector: ptrand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was pT7T3 vectod by Bento Soares and M. Fatima Bonaldo. "
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/db_xref="taxon:5691"
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1556632"
                                                                                                                                                                                                                                                                                                                 /tissue_type="carcinoid"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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76.9%;
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Pred. No. 2.5e+07;
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Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Location/Qualifiers
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19 bp mRNA linear HTC 08-JAN-20 Single read from an extremity off a full-length cDNA clone made fi Anopheles gambiae total adult females. 3-PRIME end of clone FK0AAC48CF12 of strain 6-9 of Anopheles gambiae (African malaria
                                                                                                                                                                                                                                                                                                                                              AZ500630 19 bp DNA linear GSS 05 100339A10F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0339A10 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX064981
Unpublished (2000)
Contact: Robert B.
University of Utah
                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae
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                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
                                                                                                                                                                                                                                                   Mus musculus
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/clone="FKOAAC48CF12"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"
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/strain="6-9"
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                                                                                      paired end reads from 10kb
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AZ814554.1
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Insert Length: 10000 Std Error:
Plate: 0339 row: A column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                           19 bp DNA linear GSS 20-FEB-20
2M0082P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0082P13 F, genomic survey sequence
AZ814554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 19. Location/Qualifiers
                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Rm. 308, Biomedical
                         Unpublished (2000)
Contact: Robert B.
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                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/notee="Vector: pW042nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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3.1e+07;

ches 0; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                     1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.
Large-scale Sequencing Analysis of Rice ES
Unpublished (2003)
                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                 LDA1--01-C09.g1 OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA clone HDA1--01-C09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0082 row: P column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                     CF305590.1 GI:33677351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACACAGGAAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTGCAGGAAGCGGC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC2M0082P13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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                                                                                                                                                    Kim, M.J.,
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                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. We
Contact: Utah Ge
University of Utah Ge
University of Utah
Rm. 308, Biomedical F
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: N column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ366451 20 bp DNA linear GSS 02-OCT-200 1M0115N07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0115N07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Mus musculus
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                                                                                               quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E_coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="HDA1-_01-C09"
                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0115N07"
                                                                                     organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                           Genome Center
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Laboratory Mouse DNA Resources (Accuments/Chares). The DNA (http://www.jax.org/resources/documents/chares). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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δ 밁 10 AGGAAGCG 17 σ

ORIGIN

Query Match Best Local S Matches

Similarity 8; Conserv

Conservative

<u>.</u>

Mismatches

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40.0%; Score 8; DB 8; Length 20; 100.0%; Pred. No. 3.1e+07;

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